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如如我们的有效的,我们的的的的,我们的的的的的的,我们的的的的的,我们的的的,我们的有效的的,我们的的的的,我们的的的的,我们的的的的的的。" "我们的我们的我们的我们的我们的我们的我们的我们的我们的我们的我们的我们的我们的我		
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

Fri Sep 17 21:10:05 1999; MasPar time 39.18 Seconds 1020.796 Million cell updates/sec protein - protein database search, using Smith-Waterman algorithm Psrch_pp uo v

not generated. Tabular output

>US-09-041-994-2 (1-1415) from US09041994.pep 9849 1 MSGLGENLDPLASDSRKRKL......MNMNPMPMSGMPMGPDQKYC 1415

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

77977 seqs, 28268293 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

swiss-prot37 1:swissprot Database:

Mean 56.586; Variance 121.726; scale 0.465 Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Pred. No.	9.74e-17 1.17e-18 1.17e-18 1.17e-18 1.17e-18 1.17e-18 1.17e-18 1.17e-18 1.17e-18 1.17e-18 1.17e-18 1.17e-18 1.17e-18 1.17e-18 1.17e-18 1.17e-18 1.17e-18 1.17e-18
Description	AH RECEPTOR (ARYL HYDR AH RECEPTOR (ARYL HYDR TANSCRIPTION INITIATI ARYL HYDROCARBON RECEPTRANSCRIPTION INITIATI ARYL HYDROCARBON RECEPTRANSCRIPTION REGULATOR BHYDOTHETICAL B5.0 KD FARDANGER ALPANETRACAL B33.3 KD ALPHA/BETA-GLIADIN PRE ALPHA/BETA-GLIADIN PRE ALPHA/BETA-GLIADIN PRE ALPHA/BETA-GLIADIN PRE ALPA-GLIADIN PRE ALPHA/BETA-GLIADIN PRE ALPHA/BETA-GLIADIN PRE ALPOTHETICAL PROTEIN KHOMEOBOX PROTEIN COMP-DERNDENT PROTEIN G-BOX BINDING FACTOR (ENDOTHELIAL PAS DOMAIN GLUCOSE REPRESSION MED TANNSCRIPTION REGULATON MED TANNSCRIPTION REGULATOR
SUMMARIES	AHR_MOUSE AHR_HUMAN AHR_RAT TF2D_HUMAN ARNT_DROME BTD_DROME YM38_YEAST SNF5_YEAST
BB	ананананананананан
% Query Match Length	805 848 848 848 848 848 942 1794 1794 1794 1794 1794 1794 1794 1794
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3.24 2.24 1.25e-12 2.24e-12 2.26e-12 3.26e-11 3.36e-11 3.36e-11 3.35e-11 3.35e-11 3.35e-11 3.35e-11 3.36e-12 3.36e-12 3.36e-12 3.36e-12 3.36e-12 3.36e-12 3.36e-12	1.03e-10 2.01e-10 1.44e-10
FEMALE STERILE HOMEOTI E1A-ASSOCIATED PROTEIN. CREB-BINDING PROTEIN. ALPHA/BETA-GLIADIN PRE ALPHA/BETA-GLIADIN PRE ALPHA/BETA-GLIADIN PRE POSSIBLE TRANSCRIPTION TRANSCRIPTION PACTOR R BWALL PROTEIN (MEMBER NEURONAL PAS DOMAIN PR SINGLE-MINDED HOMOLOG SINGLE-MINDED HOMOLOG SINGLE-MINDED HOMOLOG PROBABLE SERINE/THREON ATAXIN-I (SPINOCERBEEL WHITE COLLAR I PROTEIN PRESTALK-SPECIFIC PROT CREB-BINDING PROTEIN CREB-BINDING PROTEIN HYPOTHETICAL 78.0 KD P	HOMOLOG DOMAIN P IBLE FAC
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ALIGNMENTS

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MEDLINE; 94067047
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01-NOV-1995 (
15-DEC-1998 (
AH RECEPTOR (
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DOMAIN
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P41738;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                        82 FDVALKSTPADRNGGQDQCRAQ-IRDWQDLQEGEFLLQALNGFVLVVTADALVFYASSTI 140
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                                                                                                                                                                                                                                                                                                                                                                     26 PAEGIKSNPSKRHRDRLNTELDRLASLLP--FPQ-DVIN-KLDKLSVLRLSVSYLRAKSF 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-LIVER;
MEDLINE: 93347997.
ITOH S., KAMATAKI T.;
Human Ah receptor cDNA: analysis for highly conserved sequences.";
NUCLEIC ACIDS RES. 21:3578-3578(1993).
                                                                                                                                                                             AH RECEPTOR.
BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                            TRANSCRIPTION REGULATION; DNA-BINDING; REPEAT; NUCLEAR PROTEIN PROPEP {\bf 1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                         I -> M (IN DBA/2J).
H -> N (IN DBA/2J).
A -> V (IN DBA/2J).
L -> P (IN DBA/2J).
S -> N (IN DBA/2J).
L -> M (IN DBA/2J).
S -> SRGIFNETYSS (IN DBA/2J).
S -> T (IN REF. 2).
W; 1998DlAA CRC32;
                                                                                                                                                                                                                                                                                                                                   Score 232; DB 1; Length 805; Pred. No. 9.74e-17;
                                                                                                                                                                                                                                                                                                                                                    46; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (REL. 29, CREATED)
15-UUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
AH RECEPTOR (ARYL HYDROCARBON RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 848 AA
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GLN-RICH.
                                                                  PAS-1.
                                                                                                                                                                                                                  PAS-2.
                                                                                                                                                                                                                                                                                                                90337 MW;
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Best Local Similarity 30.3%;
                                                                                                                                                                                                                                                                                                                                                    46; Conservative
                                                            EMBL; D38417; G1215804; -
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                                                                                                                        PFAM; PF00785; PAC; 1.
PFAM; PF00989; PAS; 1.
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                                                                                                                                                                                                                                                                                                                805 AA;
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                                                                                                                                          TRANSFAC; T00018;
TRANSFAC; T00194;
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SEQUENCE FROM N.A.
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AHR_HUMAN
P35869;
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VARIANT
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ANTONIOU B., SMITH A., ELLIOTI G., KRAMER J.;
A ANTONIOU B., SMITH A., ELLIOTI G., KRAMER J.;
A ANTONIOU B., SMITH A., ELLIOTI G., KRAMER J.;
SEQUENCE FROM N.A.
C. I SUBMITTED (NOY-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
C. I FUNCTION: THE AH RECEPTOR ACTIVATED IN ASSOCIATION WITH A LIGAND CASCOLATION. THE AH RECEPTOR OF THE GENES BY BINDING TO THE XRE ENGLENCE IN THEIR PROMOTER REGIONS. IT MEDIATES BIOCHEMICAL AND CASCOLECTION. THEIR PROMOTER REGIONS. IT MEDIATES BIOCHEMICAL AND CASCOLECTION. FIRST CYTOPLASMIC, UPON BINDING WITH LIGAND CASCOLECTION WITH A HSP90, IT TRANSLOCATES TO THE NUCLEUS.
C. SUBUNIT. EFFICIENT DNA BINDING REQUIRES DIMERIZATION MATH AN OTHER BHLH PROTEIN. IN THE NUCLEUS, HETERODIMER OF AHR AND ARNT.
C. I SIMILARITY: CONTAINS A PAS (PERR ARNT-SIM) DIMERIZATION DOMAIN.
C. I SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
DOLWICK R.M., SCHMIDT J.V., CARVER L.A., SWANSON H.I., BRADFIELD C.A.; "Cloning and expression of a human Ah receptor cDNA."; MOL. PHARMACOL, 44:911-917(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L -> FK (IN REF. 1).
51BB7808 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA-BINDING; REPEAT; NUCLEAR PROTEIN.
BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27 PAEGIKSNPSKRHRDRLNTELDRLASLLP--FPQ-DVIN-KLDKLSVLRLSVSYLRAKSF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 PGQGLTCSGEKRRREQESKYIEELAELISANLSDIDNFNVKPDKCAILKETVRQIRQIK- 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Gaps
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(REL. 32, LAST SEQUENCE UPDATE)
(REL. 37, LAST ANNOTATION UPDATE)
(ARYL HYDROCARBON RECEPTOR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  853 AA
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PAS-2.
PAC MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIM; 600253; -.
PROSITE; PSO0038; HELIX_LOOP_HELIX; 1.
PFAM; PF00785; PAC; 1.
PFAM; PF00989; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLN-RICH.
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Local Similarity 27.5%;
hes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRANSFAC; T01795; -.
IRANSCRIPTION REGULATION;
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81
179
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85 QGKTI-SNDDDVQKADVSSTGQGVIDKDSL--GPLLLQALDGFLFVVNREANIVFVSENV 141
                                                                                                                         RESULT
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                                                                                                                                                                                                   TETRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER;

AL SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.

L SUBMITTED (JAN-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.

- I- FUNCTION: THE AH RECEPTOR ACTIVATED IN ASSOCIATION WITH A LIGAND IS CONSIDERED TO TRANSLOCATE FROM CYTOPLASM TO NUCLEUS AND ENHANCE THE TRANSCRIPTION OF THE GENES BY BINDING TO THE XRE SEQUENCE IN THEIR PROMOTER REGIONS. IT MEDIATES BIOCHEMICAL AND TOXIC EFFECTS OF HALOGENATED AROMATIC HYDROCARBONS.

- I- SUBCELLULAR LOCATION: FIRST CYTOPLASMIC, UPON BINDING WITH LIGAND CONTINUES OF THE MEDIATES TO THE UNGLEUS.

- I- SUBCELLULAR LOCATION WITH A HSP90, IT TRANSLOCATES TO THE LUNG. THYMUS > KIDNEY > LIVER. LOWER LEVEL SEEN IN HEART AND SPLEEN.

- C THYMUS > KIDNEY > LIVER. LOWER LEVEL SEEN IN HEART AND SPLEEN.

- C SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH AN OTHER CONTINUES OF THE AND ARMY.

- C SUBUNIT: SEFICIENT ON BINDING REQUIRES DIMERIZATION POWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bloinformatics and the EMED outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS A PAS (PER-ARNT-SIM) DIMERIZATION DOMAIN.
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
TRANSCRIPTION FACTORS.
                                                                                              BASIC DOMAIN.
HELLX-LOOP-HELIX MOTIF (BY SIMILARITY).
PAS-1.
PAC MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRANSCRIPTION REGULATION; DNA-BINDING; REPEAT; NUCLEAR PROTEIN;
           EUKARYOTA, METAZOA; CHORDATA, VERTEBRATA; MAMMALIA, EUTHERIA,
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISSING (IN SPLICE VARIANT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T -> S (IN REF. 2).
V -> A (IN REF. 2).
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E -> D (IN REF. 2).
G -> A (IN REF. 2).
D -> H (IN REF. 2).
Q -> H (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 239; DB 1; Pred. No. 7.91e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00038; HELIX_LOOP_HELIX; 1.
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Best Local Similarity 30.9%;
Matches 47; Conservative
(RAT)
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EMBL; U04860; G507172;
                                                            SEQUENCE FROM N.A. CTRAIN-SPRAGUE-DAWLEY;
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PFAM; PF00989; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE SPLICING DNA BIND 27
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NORVEGICUS
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CONFLICT
SEQUENCE
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RATTUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "How proteins recognize the TATA box.";
J. MOL. BIOL. 261:239-254(1996).
-!- FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION
OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II. TFIID BINDS
SPECIFICALLY TO THE TATA BOX PROMOTER ELEMENT WHICH LIES CLOSE TO
THE POSITION OF TRANSCRIPTION INITIATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Highly conserved core domain and unique N terminus with presumptive regulatory motifs in a human TATA factor (TFIID)."; NATURE 346:387-390(1990).
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 90302010.
RAO C.C., LIEBERMAN P.M., SCHMIDT M.C., ZHOU Q., PEI R., BERK A.J.;
"Cloning of a transcriptionally active human TATA binding factor.";
SCIENCE 248:1646-1649(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crystal structure of a human TATA box-binding protein/TATA element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 90326195.
HOFFWANN A., SINN E., YAMAMOTO T., WANG J., ROY A., HORIKOSHI M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 90302006.

PETERSON M.G., TANESE N., PUGH B.F., TJIAN R.;
Finctional domains and upstream activation properties of cloned human TATA binding protein.";
SCIENCE 248:1625-1630(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBUNIT: BINDS DNA AS A MONOMER.
SUBCELLULAR LOCATION: NUCLEAR.
SIMILARITY: THE C-TERMINAL 180 RESIDUES ARE EXTREMELY WELL
CONSERVED IN ALL EURARXOTIC TFIID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: WEAK, WITH BACTERIAL POLYMERASE SIGMA-FACTORS.
                                                                                                                                                                   01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
TRANSCRIPTION INITIATION FACTOR TFIID (TATA-BOX FACTOR) (TATA
                                                                                                                                                                                                                                                                                          EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 96209823.
NIKOLOV D.B., CHEN H., HALAY E.D., HOFFMANN A., ROEDER R.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JUO Z.S., CHIU T.K., LEIBERMAN P.M., BAIKALOV I., BERK A.J., DICKERSON R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                K-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 159-337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 159-339.
MEDLINE; 96346176.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROC. NATL. ACAD. SCI. U.S.A. 93:4862-4867(1996)
                                                                                                                  339 AA
141 QDYLGFQQSDVIHQSVYELIHTEDRAEFQRQL 172
                    :|| : | |::: |||;::| ||| :| :| 142 TQYLQYKQEDLVNTSVYNILHEEDRKDFLKNL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                  PRT;
                                                                                                                                                                                                                               SEQUENCE-BINDING PROTEIN) (TBP).
                                                                                                                                                     17, CREATED)
                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                    TBP OR TFIID OR TF2D HOMO SAPIENS (HUMAN)
                                                                                              ILT 4
TF2D_HUMAN STAN
'P20226;
01-FEB-1991 (REL. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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51; Indels

46; Mismatches

FDVALKSTPADRSRGQDQCRAQ-VRDWQDLQEGEFLLQALNGFVLVVTADALVFYASSTI 140

82

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26 PAEGIKSNPSKRHRDRLNTELDRLASLLP--FPQ-DVIN-KLDKLSVLRLSVTYLRAKSF 81

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MEDLINE; 94081952.
WIMMER E.A., JAECKLE H., PFEIFLE C.,
"A Drosophila homologue of human Spl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDWYGTSLYEHIHPDDREKIREQLS 150
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SEQUENCE FROM N.A.
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llarity 34.5%;
Conservative
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les 50; Conser
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DNA_BIND
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Matches
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A ELZER E., WAPPNER P., SHILO B.-Z.;

**ZELZER E., WAPPNER P., SHILO B.-Z.;

**ZENGRES E., STOOLE J. STOOLE J. STOOLE J. STOOLE D. SIM. SIM. SHILD PROTEIN. HETERODIMER WITH AHR, TRH OR SIM.

**ZELZER E., WAPPNER E., STOOLE J. STOOLE J. STACKLED HONGORDOUGLY. IN EARLY EMBRYOS,

**ZELZER E., WAPPNER E., STOOLE J. STACKLED J. S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 98040551.

OHSHIRO T., SAIGO K.;

"Transcriptional regulation of breathless FGF receptor gene by binding of TRACHEALESS/dARNT heterodimers to three central midline elements in Drosophila developing trachea.";

DEVELOPMENT 124:3975-3986(1997).
                                                                                                                                                                                                                                                                                             TRANSFAC; T00794; -.
TRANSCRIPTION REGULATION; DNA-BINDING; NUCLEAR PROTEIN; REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    015945; 016167;
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR HOMOLOG (DARNT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DROSOPHILA MELANOGASTER (FRUIT FLY).
EUKARYOTA; METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1255 QQQQQQQQQQQQQQQTQAFSPPNVTASPSMDGLLAGPTMPQAPPQQFPYQ 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 225; DB 1; Length 339;
Pred. No. 1.17e-15;
16; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQQQQQQQQQQQQQQQQQAVAAAAVQQSTSQQATQGTSGQAPQLFHSQ 125
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5D24A7B8 CRC32;
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165 241 1.
255 332 2.
58 61 M II
339 AA; 37698 MW;
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llarity 38.5%;
Conservative
                                                                                                                                                                                                                      PEAN; PEO0351; TFIID; 2.
PFAM; PF00352; TBP; 2.
TRANSFAC; T00794; -.
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M55654; G339492; -. X54993; G37066; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                      PIR; A34830; A34830.
PIR; A34831; A34831.
PDB; ITGH; O1-AUG-96.
PDB; ICDW; 23-DEC-96.
MIM; 600075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 42; Conser
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COHEN S.M.; is a head-specific segmentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> GVLRYAADVGSHADHV
                                                                                                                                                                                                                                                                                                                                                                                                     BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                   NUCLEAR PROTEIN; DNA-BINDING; TRANSCRIPTION REGULATION; ACTIVATOR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
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EUKAKOTA: METAZOA; ARTHROPODA: TRACHEATA; HEXAPODA; INSECTA;
PTERYGOTA: DIPTERA: BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
PROSOPHILIDAE: DROSOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NATURE 366:690-694(1993).
-i- FUNCTION: REQUIRED FOR THE DEVELOPMENT OF THE ANTENNAL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 642;
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POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-PRO.
M -> V (IN REF. 2).
Q -> QQO (IN REF. 2).
P -> T (IN REF. 2).
P -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EFSDMLQMLDHTPTTFEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 224; DB 1;
Pred. No. 1.67e-15;
39; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IN REF. 2).
983D5207 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAS-1.
PAS-2.
PAC MOTIF.
                                                                                                                                                                                  EMBL; AB002556; D1023738; -.
EMBL; AF016053; G2367597; -.
FLYBASE; FBG010015014; tgo.
PROSITE; PS00038; HELIX_LOOP_HELIX; 1.
PFAM; PF00010; HUH; 1.
PFAM; PF00989; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-ARG.
POLY-ALA.
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EMBL; Z49705; G825569;

HYPOTHETICAL PROTEIN

290

DOMAIN

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INTERCALARY AND MANDIBULAR SEGMENTS OF THE HEAD.

-!- DEVELOPMENTAL STAGE: FIRST EXPRESSED IN A STRIPE COVERING THE HEAD ANLAGEN OF THE SYNCITIAL BLASTODERN EMBRYO, PERSISTS THROUGH GASTRULATION AND DECAYS DURING GERM BAND EXTENSION. EXPRESSED LATER IN DEVELOPMENT IN A COMPLEX SPATIALLY RESTRICTED PATTERN.
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1211 QPQQGFLNAQMYAQRSRELLSHHFRQQRVAMMQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EURARYOTA: FUNGI: ASCOMYCOTA: HEMIASCOMYCETES; SACCHAROMYCETALES;
                                                                                                                                                                                                                                   PROSITE; PS00028; ZINC_FINGER_C2H2; 3.
PFAM; PF00096; zf-C2H2; 3.
HSSP; P08047; 1SP2.
TRANSCRIPTION REGULATION; ACTIVATOR; ZINC-FINGER; METAL-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 85.0 KD PROTEIN IN HLJ1-SMP2 INTERGENIC REGION.
YMR164C OR YM8520.13C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.99e-16;
19; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265D561A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 230; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   758 AA.
                                                                                                                                                                                                                                                                                                          ZINC-FINGERS.
                                                                                                                                                                                                                                                                                                                       C2H2-TYPE.
C2H2-TYPE.
C2H2-TYPE.
GLM-RICH.
POLY-ALA.
POLY-PRO.
POLY-PRO.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1270 -AF-SPPRNVTASPSMDGLLAGPTMPQAP 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 HDFLSAAALLSAPPSLSGSSSGSSG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SACCHAROMYCETACEAE; SACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68581 MW;
                                                                                                                                                                                                                                                                                             PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 48.3%;
Matches 43; Conservative
                                                                                                                                                                                                         EMBL; Z29361; G441284; -. FLYBASE; FBgn0000233; btd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                    502
519
536
599
                                                                                                                                                                                                                                                                                                                                    385
                                                                                                                                                                                                                                                                                           NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           644 AA;
                                                                                                                                                                                                                                                                                           DNA-BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YM38_YEAST
Q03825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                       ZN_FING
ZN_FING
                                                                                                                                                                                                                                                                                                                                                    ZN_FING
                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
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SEQUENCE FACE
STRAIN-S28G M.A.;
HUNT S., BORWAN S., BARRELL B.G., RAJANDREAM M.A.;
SUBMITTED (MAY-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.

SEQUENCE FROM N.A.

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                                                                                                                                                                             ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSCRIPTION REGULATORY PROTEIN SNFS (SWI/SNF COMPLEX COMPONENT SNFS) (TRANSCRIPTION FACTOR TYE4). SNFS OR TYE4 OR SWI10 OR YBR289W OR YBR2036.
                                                                                                                                                                                                                                             1211 OPQGGFLNAQMVAQRSRELLSHHFRQQRVAMMMQQQQQQQQQQQQQQQQQQQQQQQTQ- 1269
                                                                                                                                                                                                              MEDLINE; 94378722.

HOLMSTROEM K., BRANDI I., KALLESOE I.;
HOLMSTROEM K., BRANDI I., KALLESOE I.;
HOLMSTROEM K., BRANDI I., KALLESOE I.;
The sequence of a 32,420 bp segment located on the right arm of chromosome II from Saccharomyces cerevisiae.";
YEAST 10:547-S62(1994).
-!- FUNCTION: INVOLVED IN TRANSCRIPTIONAL ACTIVATION. THE SWI/SNF COMPLEX IS REQUIRED FOR THE INDUCED EXPRESSION OF A LARGE NUMBER OF GENES. THIS COMPLEX ALIERS CHROMATIN STRUCTURE TO FACILITATE BINDING OF GENE-SPECIFIC DEDICATED TRANSCRIPTION FACTORS.
-!- SUBUNII: COMPONENT OF THE SWI/SNF GLOBAL TRANSCRIPTION ACTIVATOR
                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAURENT B.C., TREITEL M.A., CARLSON M.; The SNF5 protein of Saccharomyces cerevisiae is a glutamine- and proline-rich transcriptional activator that affects expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
SACCHAROMYCETACEAE; SACCHAROMYCES.
                                                                                                                                                                               4;
                                                                                                                                        Length 758;
                                                                                                                                      Score 227; DB 1; Length 758,
Pred. No. 5.77e-16;
16; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSCRIPTION REGULATION; ACTIVATOR; NUCLEAR PROTEIN.
                                                                                                                                                                                                                                                                                                                   1270 AFSPPDNVTASPSMDGLLAGPTMPQAPP--QQFPYQPNYGM 1308
                                                                                                                                                                                                                                                                                  333 PIVNPQMVPHIPSENSHSTG-LMPSVPPTNQQFNAQTQSSM 372
                                                                                                       F09544CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (REL. 16, CREATED)
01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                         905 AA
                                                                    POLY-ASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               broad spectrum of genes.";
MOL. CELL. BIOL. 10:5616-5625(1990).
                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                     85050 MW;
                                                                                                                                      Query Match 2.3%;
Best Local Similarity 44.6%;
Matches 45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M36482; G172638; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 236158; G536742; -
                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                   329
637
656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S39145.
                                                                605
653
758 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S44551; RGBYS5.
PIR; S39145; S39145.
SGD; L0001948; SNF5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 91042489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                       SNF5_YEAST
P18480;
                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X7
                                                                    DOMAIN
                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                       RESULT
STITES
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                                                                                                                                                                                                                                                                                                                                                                                    Gaps 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1117 AQGPPMQGGFHLQGQSPSFNSMMNQMNQQGNFPLQGM-HPRANIMRPRINTPKQLRMQL- 1174
                                                                                                                                                                                                                                                                                                                                                                                                                                               113 GQVPLAPAPINLPPQIAQL-PLATQQQVLNKLRQQAIAKNNPQVVNAITVAQQQVQRQIE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HARRIS D., MCDONALD S., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.; SUBMITTED (FEB-1996) TO EMBL/GENBANK/DDBJ DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 QQKGQQTAQTQLEQQRQLL-VQQQQQQLRNQIQRQQQQQFRHHVQIQQQQQKQQQQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MCLEAN J., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUBMITTED (APR-1996) TO EMBL/GENBANK/DDBJ DATA BANKS
-1- SIMILARITY: SOME, TO YEAST PANI AND TO MAMMALIAN EPSI5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 229; DB 1; Length 1794;
Pred. No. 2.84e-16;
55; Mismatches 142; Indels 34;
                                                                                                                                                                                                                                                                                                                                                                                    86; Indels 10;
                                                                                                                                                                                                                                                                                                                  Length 905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (REL. 34, CREATED)
01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
RYPOTHETICAL 193.3 KD PROTEIN C27F1.01C IN CHROMOSOME
SPAC27F1.01C OR SPAC25G10.09C.
GLN-RICH.
PRO-RICH.
PRO-RICH.
ASP/GLU-RICH (ACIDIC).
PRO-RICH.
ARG/LVS-RICH (BASIC).
E -> D (IN REF. 1).
E -> D (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA; ARCHIASCOMYCETES;
SCHIZOSACCHAROMYCETALES; SCHIZOSACCHAROMYCETACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 270691; E1168610; -.
HYPOTHETICAL PROTEIN; REPEAT.
SEQUENCE 1794 AA; 193279 MW; F5418320 CRC32;
                                                                                                                                                                                                                                                                                                           Score 226; DB 1;
Pred. No. 8.23e-16;
                                                                                                                                                                                                                                                                                                                                                                                    42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1794 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1457-1794 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1291 TMPQAPPQOFPYQPNYGM 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-1748 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 TNVQPTIGQLPQLPKLNL 306
                                                                                                                                                                                                                                                102557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.3%;
Best Local Similarity 29.4%;
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                  Query Match 2.3%;
Best Local Similarity 30.3%;
                                                                                                                                                                                                                                                                                                                                                                                    60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z69368; E221304;
                                                                                                                                                                                                      564
905 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHIZOSACCHAROMYCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XAV1_SCHPO
Q10172;
                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                         CONFLICT
                                                                            DOMAIN
                                                                                                                                       DOMAIN
                                                                                                           DOMAIN
                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                Matches
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394 QQMAAQMFGGFQQAAGIPSQIIGFQPQAMMPQRIGMQPQMIGFQQPMIPQRIGMQPQMIG 453

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                                                                                                                                                        1331 MG-PSONPMMOHPQAASIYOSSEMKGWPSGNLARNSSFSOOOFAHOGNPAVYSMV-HMNG 1388
                                                                                                 1105 DQKAG-LYGQTYPAQGPPMQ-GGFHLQGQSPSFNSMMNOMN--QQGNFPLQ-GMHPRANI 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 RVPVPQLQPQNPSQQQPQEQVPLVQQQQFLGQ-QQPFPPQQPYPQPQPFPSQQPYLQLQP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    TRITICUM AESTIVUM (WHEAT).
EUKARYOTA: VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
                                                     1160 MRPRINIPKQLRMQLQQRLQG-QQFLNQSRQALELKMENPIAGGAAVMRPMMQPQQ-GFL
                                                                                  QQPMVPQRTGMQPMMPGLQQPMAPQRTGMQPMMPQRTGMQPQMTGFQQPMAPQRTGMQPM
                                                                                                                                       569 MPQRTGMO-PQMPGMQQ-PMAPQRTGMQ-PMMPQRTGM-QQPMAP-QRTGMQP--MMPQR
                                                                                                                                                                                              622 TGMQPQMPGMQQPMAPQRTGMQPMMPQRTGMQPQMPGM-QQPMAPQ-RTGMQPMAPQRTG
                           FOOPM-MP-Q-RIGLOPOMIGFOOPMVPORIGMOPOMIGFOOPMMP-ORIGLOPOMIGF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M11074; G170722; -.
PIR; B22364; B22364.
SEED STORAGE PROTEIN; REPEAT; SIGNAL; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALPHA/BETA-GLIADIN A-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 219; DB 1;
Pred. No. 9.70e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229A083D CRC32;
                                                                                                                                                                                                                                                                                                                                                              (REL. 05, CREATED)
(REL. 05, LAST SEQUENCE UPDATE)
(REL. 16, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Mismatches
                                                                                                                                                                                                                                                                                                                                     262 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 219;
                                                                                                                                                                                                                                                                              1389 SSGHMGQMN-MNPMPMSGM--PMGPDQ 1412
                                                                                                                                                                                                                                                     680 MQPMMPQRTGMQP-QMPGMQQPMAPQR 705
                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 AA; 30403 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 31.6%;
nes 50; Conservative
                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262
                                                                                                                                                                                                                                                                                                                                                                                                                                                              POACEAE; TRITICUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85234522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                               13-AUG-1987
13-AUG-1987
                                                                                                                                                                                                                                                                                                                       LT 10
GDA1_WHEAT
P04721;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
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526 PPSHHHHPHHQAAPSPG-AAAASASMLHHNHHLLYHPAAQHHPPSDWYHTTAPSG-SAE 583
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ZN_FING
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ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1155 PRANIMRPRINTPK-QLRMQLQQRLQCQQFLNQSRQALELKMENPTAGGAAVMRPMMQPQ 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1214 QGFLNAQMVAQRSRELLSHH-FRQQRVAMMMQQQQ-QQQQQQQQQQQQQQQQQQQQQTQAF 1271
1215 GFLNAQMVAQRSRELLSHH-FRQQRVAMMMQQQQQQQQQQQQQQQQQQQQQQQQQQQTQAFSP 1273
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                                                                                                                                                                                                                                    EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;
EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; LILIOPSIDA; POALES;
POACEAE; TRITICUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 313 ALPHA/BETA-GLIADIN (CLONE PW8142).
313 AA; 36118 MW; 903855A1 CRC32;
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9
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EUKARYOTA; META2OA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70; Indels
                                                                                                                                               ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLONE PW8142).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00234; tryp_alpha_amyl; 1.
SEED STORAGE PROTEIN; REPEAT; SIGNAL; MULTIGENE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1272 SPPPNVTASPSMDGLLAGPTMPQAPPQQFPYQPNYGMGQQ 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 QQILQQQLIPCRDVVLQQHNIAHASSQVLQ-QSTYQLLQQ 179
                                            1274 PPNVTASPSMDGLLAGPTMPQAPPQQFPYQPNYGMGQQ 1311
                      139 ILQQQLIPCMDVVLQQHNIVHGKSQVLQ-QSTYQLLQE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 3,93e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.2%; Score 215; DB 1;
                                                                                                            (REL. 05, CREATED)
(REL. 05, LAST SEQUENCE UPDATE)
(REL. 16, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995 (REL. 31, CREATED)
01-FEB-1995 (REL. 31, LAST SEQUENCE UPDATE)
01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
01-FEB-1996 (REL. 30, LAST ANNOTATION UPDATE)
                                                                                          313 AA.
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                                                                                                                                                            (WHEAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 31.9%;
nes 51; Conservative
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                                                                                         STANDARD:
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                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 85242077. SUMNER-SMITH M., R.
                                                                                                                                                            TRITICUM AESTIVUM
                                                                                                                                     01-NOV-1990 (REL.
                                                                                                              13-AUG-1987
                                                                                                                         13-AUG-1987
                                                                                       GDA7_WHEAT
P04727;
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OPA_DROME
P39768;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLUIAR LOCATION: NUCLEAR (PROBABLE).
DEVELOPMENTAL STAGE: THE PEAK EXPRESSION IS SEEN BETWEEN 2 AND 12 HR OF EMBRYOGENESIS. EXPRESSION CONTINUES THROUGH THE LARVAL INSTARS AND DURING PUPATION ALTHOUGH AT LOWER LEVELS COMPARED WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL PROTEIN; PAIR-RULE PROTEIN; ZINC-FINGER; METAL-BINDING; DNA-BINDING; REPEAT; NUCLEAR PROTEIN; TRANSCRIPTION REGULATION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BENEDYK M.J., WULLEN J.R., DINARDO S.; "Odd-paired: a zinc finger pair-rule protein required for the timely activation of engrailed and wingless in Drosophila embryos."; GENES DEV. 8:105-117(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                    -I- FUNCTION: TRANSCRIPTION FACTOR ESSENTIAL FOR PARASEGMENTAL SUBLYISION OF THE DROSOPHILA EMBRYO. IT IS INVOLVED IN THE ACTIVATION OF WINGLESS (WG) IN ODD PARASEGMENTS. IT IS ALSO REQUIRED FOR THE TIMELY ACTIVATION OF WG IN THE REMAINING PARASEGMENTS AND FOR THE TIMELY ACTIVATION OF ENGRALLED (EN) IN
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SIMILARITY: TO THE GLI-RELATED GROUP OF C2H2-TYPE ZINC-FINGERS
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CIMBORA D.M., SAKONJU S.;
"Drosophila midgut morphogenesis requires the function of
segmentation gene odd-paired.";
DEV. BIOL. 169:580-595(1995).
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PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROIDEA;
DROSOPHILIDAE; DROSOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ATYPICAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0E93A977 CRC32;
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C2H2-TYPE.
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PROSTIE: PSG0028; ZINC_FINGER_C2H2; 3.
PFAM; PF00096; zf-C2H2; 4.
HSSP; P08047; 1SP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALA-RICH.
POLY-HIS.
POLY-SER.
SER-RICH.
SER-RICH.
GLN-RICH.
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Local Similarity 28.7%;
Local Similarity 28.7%;
Local Similarity 28.7%;
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EMBL; S78339; G994859; -
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567
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291
321
351
609 AA;
                                                                                 N.A.
                                                                                                                MEDLINE; 94116854
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                                                                                    SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99; Indels 17; Gaps 14;
                                                                                                   TISSUE SPECIFICITY: DETECTED IN MANY CELLS IN THE CENTRAL NERVOUS SYSTEM, ALL EXTERNAL SENSORY ORGANS, SOME PERIPHERAL NEURONS, AND IN THE NON-NEURAL CELLS OF THE SPIRACLES AND THE MALPIGHIAN
                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE: CELL-SPECIFIC PATTERN OF EXPRESSION. BROADLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSFAC; T02004; -.
HOMEOBOX; DNA-BINDING; DEVELOPMENTAL PROTEIN; NUCLEAR PROTEIN;
                                                                                                                                                                                                                                                                                                                                                                                      -! - SIMILARITY: TO MAMMALIAN CCAAT DISPLACEMENT PROTEIN (CDP).
                                     EUKARYOTA; METAZOA; ARTHROPODA; TRÁCHEATA; HEXAPODA; INSECTA;
PTERYGOTA; DIPTERA; BRACHYCERA; MUSCOMORPHA; EPHYDROLDEA;
DROSOPHILIDAE; DROSOPHILA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 217; DB 1; Length 2175;
Pred. No. 1.96e-14;
77; Mismatches 99; Indels 1
                                                                                                                                                                                                                                                                                                                                 EXPRESSED DURING EMBRYONIC DEVELOPMENT.
DOMAIN: ASN AT POSITION 47 OF THE HOMEOBOX MAY PARTICIE
REGULATING DNA-BINDING ACTIVITY BY PROMOTING HOMO- AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALA-RICH.
HIS/GLN-RICH (OPA-REPEAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COILED COIL (POTENTIAL).
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC).
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ASP/GLU-RICH (ACIDIC).
ALA/PRO-RICH.
W; D7E1FC12 CRC32;
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ASP/GLU-RICH (ACIDIC).
ASN-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CUT'-REPEATS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALA/GLN-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOMEOBOX
                           DROSOPHILA MELANOGASTER (FRUIT FLY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FLYBASE; FBGN0004198; ct.
PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X07985; G7768; -.
EMBL; X07985; E1808; ALT_SEQ.
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Similarity 23.1%;
58; Conservative
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HSSP; P04002; lWFA.
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1689
1804
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 HOMEOBOX PROTEIN CUT.
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Best Local Similarity
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SEQUENCE FROM N.A.
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DNA_BIND
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SEQUENCE
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2003 QQQQQQQQQQQQQQQQQXHIRQQQQQILRQQQQQQQQQQQQQQQQQQQQQQQQQQQ
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م
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TISSUB-BONE MARROW;
MEDILS, 96281124.
MEDILS: 96281124.
NAGASE T., SEXI N., ISHIKAWA K.-I., TANAKA A., NOMURA N.;
"Prediction of the coding sequences of unidentified human genes."
"The coding sequences of 40 new genes (KIRA0161-KIRA0200) deduced hanalysis of cDNA clones from human cell line KG-I.";
DNA RES. 3:17-24(1996).
-i- TISSUE SPECIFICITY: UBIQUITOUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ï
                                                                                                                                                                                                                       EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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Pred. No. 7.89e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW; 24317D02 CRC32;
                                                                                                                                           01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
101-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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POLY-GLY.
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POLY-GLN.
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Best Local Similarity 34.7%;
                                                              1360 NLARNSSFSQOOFAHQ 1375
                                     584 АМИРІЛНЕСНИНННН 599
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                                                                                                                    STANDARD;
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01-MAR-1989
01-FEB-1996
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P10180;
                                                                                                                    HUMAN
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PARTICIPATE IN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAT. GENET. 8:221-228(1994).

-!- POLYMORPHISM: THE POLY-GLN REGION OF THE MACHADO-JOSEPH PROTEIN IS HIGHLY POLYMORPHIS. THE POLY-GLN REPEATS IN THE NORMAL POULLATION AND HIGHLY POLYMORPHIS. THE POLY SEASON ABOUT 68-82 REPEATS IN MJD1 PATIENTS. LONGER EXPANSIONS RESULT IN EARLIER ONSET AND MORE SEVERE CLINICAL MANIFESTATIONS OF THE DISEASE.

-!- DISEASE: DEFECTS IN MJD1 ARE THE CAUSE OF MACHADO-JOSEPH DISEASE (MJD), A NEURODEGENERATIVE DISORDER CHARACTERIZED BY CEREBELLAR ATAXIA, PYRAMIDAL AND EXTRAPYRAMIDAL SIGNS, PERIPHERAL NERVE PALSY, EXTERNAL OPHTALMOPLEGIA, FACILAL AND LINGUAL FASCICULATION AND BULGING. THIS DISEASE IS AUTOSOMAL AND DOMINANT, WITH A LATE ONSET OF SYMPTOMS, GENERALLY AFTER THE FOURTH DECADE.
                        1477 MSAAMQQQQVAQAQQQAQQAQQAQQAQQHLQQQQHLQQQQHLAQQQHPHQQHHQA-AAAAA 1535
                                                                                                                                                                                              1277 VTASPSMDGLLAGPTMPQAPPQQFPYQPNYGMGQQPDPAFGRVSS-PPNAMMSSRWGPSQ 1335
                                                                                                                                                                                                                                                       1592 GTNAMRSLHQHMSPTVYEMAALTQ-DLDTHDITTKIKEALLANNIGQKIFGEAVLGLSQG 1650
1422 KLMRTGSYSGSPQMPQGLASKMQAASLPMQKMMS-ELKLQEPAQA-QHLMQQM-QAA-A- 1476
                                                                                                                                                                     1536 ALHHQSM--LLTSPGLP--PQHAISLPPSAGGAQPGGPGGNQGSSNPSNSEKKPMLMPVH 1591
                                                                                                                                                                                                                                                                               |:| |: ::::|: | |: 1336 --NPMQ-HPQ-AASIYQSSEMKGWPSGNLARNSSFSQQQFAHQGNPAVYSMVHMNGSSG 1391
                                                                                                              TISSUE-BRAIN;
MEDLINE; 93179166.
MEDLINE; 93179166.
KARAGUCHI Y., OKAMOTO T., TANIWAKI M., AIZAWA M., INOUE M.,
KATAYAMA S., KAWAKAMI H., NAKAMURA S., NISHIMURA M., AKIGUCHI I.,
KATAYAMA S., KAKIZUKA A.;
"CAG expansions in a novel gene for Machado-Joseph disease at
chromosome 14q32.1.";
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PRIMATES; CATARRHINI; HOMINIDAE; HOMO.
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7A909182 CRC32;
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01-0CT-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CT-1996 (REL. 34, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360 AA.
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P54252;
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2.1%; Score 210; DB 1; Length 360; 14.4%; Pred. No. 2.23e-13; ttive 14; Mismatches 33; Indels

Best Local Similarity 44.4%; Matches 40; Conservative

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Query Match

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Search completed: Fri Sep 17 21:12:04 1999

Job time : 119 secs

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Fri Sep 17 21:12:20 1999; MasPar time 80.13 Seconds 963.760 Million cell updates/sec MPsrch_pp

Tabular output not generated.

>US-09-041-994-2 1-1415) from US09041994.pep 9849 1 MSGLGENLDPLASDSRKRKL......MNNNPMPMSGMPMGPDQKYC 1415

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

179066 seqs, 54579741 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

sptremb19 Database:

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human 5:sp_lnvertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle 9:sp_bhage 10:sp_plant 11:sp_rodent 12:sp_unclassified 13:sp_vertebrate 14:sp_virus

scale 0.456 Mean 54.229; Variance 118.858; Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length DB	DB	Ð	Description	Pred. No.
1	7640	77.6	1398	=======================================	000600	NUCLEAR RECEPTOR COACT	0.00e+00
7	6892	70.0	1391	13	057539	RETINOID X RECEPTOR-IN	0.00e+00
m	3346	34.0	1464	4	015596	TRANSCRIPTIONAL INTERM	0.00e+00
4	3300	33.5	1462	7	061026	GRIP1.	0.00e+00
'n	2887	29.3	1463	Ξ	00600	NUCLEAR RECEPTOR COACT	0.00e+00
9	1852	18.8	326	7	015406	CAGH16.	0.00e+00
7	1696	17.2	1398	7	043793	STEROID RECEPTOR COACT	2.28e-286
80	1696	17.2	1440	7	043792	STEROID RECEPTOR COACT	2.28e-286
6	1691	17.2	1441	7	000150	STEROID RECEPTOR COACT	2.08e-285
10	1674	17.0	1405	11	P70366	NUCLEAR RECEPTOR COACT	3.83e-282
11	1665	16.9	1405	Π	061202	NUCLEAR RECEPTOR COACT	2.05e-280
12	1642	16.7	1447	Ξ	P70365	NUCLEAR RECEPTOR CO-AC	5.31e-276
13	643	6.5	1061	4	Q13420	STEROID RECEPTOR COACT	1.07e-87
14	376	3.8	416	4	013071	(HIN-2).	2.68e-40
15	267	2.7	579	4	060657	TPA INDUCIBLE PROTEIN.	3.35e-22
16	232	2.4	232	7	Q13804	AROMATIC HYDROCARBON R	1.06e-16
17	232	2.4	349	7	014516	CLOCK (FRAGMENT).	1.06e-16
18	232	2.4	357	10	004365	OMEGA SECALIN.	1.06e-16
19	240	2.4	810	11	088930	ARYL HYDROCARBON RECEP	6.13e-18
20	240	2.4	815	11	089105	ARYL HYDROCARBON RECEP	6.13e-18

1.06e-16	1.25e-17	3.66e-17	7.46e-17	2.56e-15	3.63e-15	1.26e-15	2.16e-16	3.08e-16	6.25e-16	3.08e-16	6.25e-16	6.25e-16	6.25e-16	3.63e-15	8.89e-16	4.39e-16	1.52e-16	1.52e-16	1.04e-14	4.18e-14	8.35e-14	8.35e-14	8.35e-14	5.15e-15
CLOCK.	AH RECEPTOR (ARYL HYDR	CIRCADIAN LOCOMOTER OU	PROTEIN KINASE YAKA.	CAGH44 (FRAGMENT).	ALPHA/BETA-GLIADIN STO	TRANSCRIPTION INITIATI	SEC1 PRECURSOR.	OMEGA SECALIN PRECURSO	BASIC HELIX-LOOP-HELIX	GLUTAMINE-ASPARAGINE R	AROMATIC HYDROCARBON R	BRAIN CYCLIC NUCLEOTID	HYPERPOLARIZATION-ACTI	SIMILARITY TO DROSOPHI	KIAA0181 PROTEIN (FRAG	T05A10.1 PROTEIN.	ALR.	ALR.	ALPHA-GLIADIN.	ALPHA-GLIADIN STORAGE	CAGH45.	MASTERMIND.	OPA-CONTAINING PROTEIN	SIMILAR TO ZINC FINGER
015516	002747	008785	044011	015409	041546	016845	043639	005573	044082	023847	073772	054899	088704	P91094	014686	022190	014687	014686	041509	041529	015410	024754	075557	Q22463
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                           EFIGLMRTRDKKAPYILIVRMLMKT-HDILEDVNASPETRORYETMOCFALSOPRAMLEE
                                                                                 RCIQRFFSLNDGQSWSQKRHYQEAYVHGHAETPVYRFSLADGTIVSAQTKSKLFRNPVTN
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01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
RETINOID X RECEPTOR-INTERACTING COACTIVATOR XICO.
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: AMPHIBIA: BATRACHIA: ANURA;
MESOBATRACHIA: PIPOIDEA; XENOPODINAE: XENOPUS.
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QALDGFLYVVNREGSIVFVSENVTQYLQYKQEDLVNTSVYSILHEEDRKDFLKNLPKSTV
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KIM H.-J., LEE S.-K., NA S.-Y., CHOI H.-S., LEE
MOL. ENDOCRINOL. 0:0-0(1998).

EMBL. AF044080; G2852394; -.

SEQUENCE 1391 AA; 152532 MW; C1426F5D CRC32;
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DT 01-7UN-1998 (7)

DT 01-7UN-1998 (7)

DE NOT-1998 (7)

DE NOT-1998 (7)

DE RETINOID X REB

CC ENKARYOTA: ME

CC MESOBATRACHIA

RN [1]

RR KIM H.-J., LEB

RR KIM H.-J., L
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CATARRHINI; HOMINIDAE; HOMO.
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LSSLSSPGQKVENNSNMNMPQQGKICNQDCKSPSGLYCEQGQVESSVCQSSGREHLGEKD
                               VKENIFEGSESQRSQAESKGHKKLLQLLTCFTEERGQSLMSSSSMD--CKDSS-NVTSPS
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Q15596 PRELIMINARY;
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01-NAY-1997 (TREMBLREL. 0:
01-NOV-1998 (TREMBLREL. 0:
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MEDLINE; 96312964.

WEDLINE; 96312964.

VORGEL J.J., HEINE M.J.S., ZECHEL C., CHAMBON P., GRONEMEYER H.;

"TIF2, a 160 kba transcriptional mediator for the ligand-dependent activation function AF2 of nuclear receptors.";

EMBO J. 15:3667-3675(1996).

EMBL; X97764; ES07031; -

PFRM; PF00989; PAS; 1.

SEQUENCE 1464 AA; 159156 MW; C761519D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GMNPGQPTSMLSPRHRMSPGVAGSPRIPPSQFSPAGSLHSPVGVCSSTGNSHSYTNSSLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                          177 TVNGVSWINEPQRQKSHTFNCRMIMKTPHDILEDINASPEMRQRYETMQCFALSQPRAMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEGEDIQSCMICVARRITIGERIFPSNPESFITRHDLSGKVVNIDINSLRSSMRPGFEDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|: :: | | |: :| | |: :| | || || PSSRAYGLADPSTTGQMSGARYGGSSNIASLTFQPGPGMQSPSSYQNNNYGLNMSSPPHGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSPLASS-LSDINKDSTGSL--P-G----SG---ST---HGTSLKEKHKILHRLLQDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQLPQLFPDTRPGAPAGSVDKQAIINDLMQLTAENSPVTPVGAQKTALRISQSTFNNPRP
                                                                                                                                                                                                                      1 MSGMGENTSDPSRAETRKRK-ECPDQLGPSPKRNTEKRNREQENKYIEELAELIFANFND
                                                                                                                                                                                                                                                                                                                                                         LEALDGFFFVVNLEGNVVFVSENVTQYLRYNQEELMNKSVYSILHVGDHTEFVKNLLPKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRRCIQKFHAQHEGESVSYAKRHHHEVLRQGLAFSQIYRFSLSDGTLVAAQTKSKLIRSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSNINFPINGPKEQMGMPMGRFGGSGGMNHVS---GMQATTP-QGSNYALKMNSPSQSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEGEDLQSCLICVARRVPMKERPVLPSSESFTTRQDLQGKITSLDTSTMRAAMKPGWEDL
                                                                                                                                                                                   Indels 139;
                                                                                                                                                  Length 1464;
                                                                                                                                                 34.0%; Score 3346; DB 4; I. Larity 44.1%; Pred. No. 0.00e+00; Conservative 370; Mismatches 318;
                                                                                                                                                                    Similarity
653; Conser
                                                                                                                                                      Query Match
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                                                                                                                                                                     Best Loca
Matches
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MUS MUSCULUS (MOUSE).
EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GQ--RPSYATLR-MQPRPG-LRPTGLVQNQPNQLRLQLQHRLQAQQ--N--RQPL-MNQ 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           960 TLPLRSNSIPGARPVLQQQQMLQMRPGEIPMGMGANPYGQA-AASNQLGSWPDGMLSME 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PELVSQSQAVDPEQ--FSSQDSNIMLEQKAPVFPQQYASQAQMAQGSYS-PMQDPNFHTM 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QASFASQNRQPFGSSPDDLLCPHPAAESPSDEGALLDQLYLALRNFD--GLEEIDRALGI 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---MRPSSQPGQRQTLQSQV-M-NIGPSELEMNMGGPQYSQQQAPPNQTAPWPESILPID 1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1315 FTGATTPQSPLMSPRMAHTQSPMMQQSQANPAYQAPSDINGWAQGNMGGNSMFSQQSPPH 1374
                                                                                                                                                                                                                                                   SMGGPNRNVTVTQTPSSGDWGLPNSKAGRME-PMNSNSMGRPGGDYNTSLPRPALGGSIP 959
                                                                                                    SSTGMIGNSASRPIMPSGEWA-PQSSAVRVTCAATTSAMNRPV-Q-G-GMIRNP-AASIP 989
S--SDFYNNSIS-S-NGS---H--LGT-KQ---Q---VFQ-GINSLGLKSSQSV-QSIRP 850
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HONG H., KOHLI K., GARABEDIAN M.J., STALLCUP M.R.;
HONG H., KOHLI K., GARABEDIAN M.J., STALLCUP M.R.;
HONG H., KOHLI K., GARABEDIAN M.J., STALLCUP M.R.;
Gomain of transcriptional coactivator for the AF-2 transactivation
domain of steroid, thyroid, retinoid, and vitamin D receptors.";
MOL. CELL. BIOL. 17:2735-2744(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1210 ISNVSNVNLTLRPGV-PTQAPINAQMLAQRQREILNQHLRQ-R-QM-----HQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QQQVQQRTLMMRGQGLNMTPSMVAPSGMPATMSNPRIPQANAQQFPFPPNYGISQQPDPG
                                                                  GQLGRLLPNQNLPLDITLQSPTGAGPFPPIRNSSPYSVIPQPGMMG-NQGMIGNQGNLGN
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STRAIN-ICR OUTBRED; TISSUE-BRAIN;
MEDLINE; 96209838.
HONG H., KOHLI K., TRIVEDI A., JOHNSON D.L., STALLCUP M.R.;
"GRIP1, a novel mouse protein that serves as a transcriptional coactivator in yeast for the hormone binding domains of steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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STRAIN-ICR OUTBRED; TISSUE-BRAIN;
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061026; P97759;
01-NOV-1996 (TREMBLREL: 0
01-JAN-1998 (TREMBLREL: 0
01-NOV-1998 (TREMBLREL: 0
GRIPI:
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                                                                                                                                                                                                                                                                                                                                                                                                                            LVRRCIQKFHTQHEGESLSYAKRHHHEVLRQGLAFSQIYRFSLSDGTLVAAQTKSKLIRS 358
                                                                                                                                                                                                                                                                                                                                                                                                                                        PYTNDRHGEVSTHFLQREQNGYRPNPVPVGQGI-RP--PWAGCNSSVGGM-SMSPNQGLQ 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AKLTAEATGKELSQESSSTAPGSEVTVKQEPASPKKKEN-ALLRYLLDKDDTKDIGLP-E 761
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                                                                                                                                                                                              1 MSGMGENTSDPSRAETRKRK-ECPDQLGPSPKRSTEKRNREQENKYIEELADLIFANFND
                                                                                                                                                                                                          LEALDGFFFVVNLEGSVVFVSENVTQYLRYNQEELMNKSVYSILHVGDHTEFVKNLLPKS
                                                                                                                                                                                                                                                                                                   EEGEDLQSCLICVARRVPMKERPTLPSS-ESFTTRQDLQGKITSLDTSTMRAAMKPGWED
                                                                                                                                                                                                                                                                                                                                                                                          QTINEPQLVISLHMLHREQNVCVMNPDLTGQAMGKPLNPISSSSPAHQALCSGNPGQDMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGMNPGQASSVLSPRQRMSPGVAGSPRIPPSQFSPAGSLHSPVGVCSSTGNSHSYTNSSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 129;
                                                                                                                                               Length 1462;
                                          SEQUENCE FROM N.A.
STRAIM-ICR OUTBRED: TISSUE-BRAIN;
SUBMITTED (FEB-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; U39060; G1853980;
EMBL; U39060; G1853980;
MGD; MGL:107429; GRIPJ.
PFAM; PF00989; PAS; 1.
                       BANKS
                                                                                                                                              ch 33.5%; Score 3300; DB 11;
L Similarity 42.8%; Pred. No. 0.000+00;
631; Conservative 375; Mismatches 339;
                                                                                                                         1462 AA; 158511 MW; 9F9EC6A7 CRC32;
                       DATA
STRAIN=ICR OUTBRED; TISSUE=BRAIN;
STALLCUP M.R.;
SUBMITTED (OCT-1995) TO EMBL/GENBANK/DDBJ
                                                                                                                         SEQUENCE
                                                                                                                                                 Query Match
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Matches
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SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                            ANSQPGQRQMLQSQV-M-NIGPSELEMNMGGPQYNQQAPPNQTAPWPESILPIDQASFA 1049
                                                                                                                                                                                                                                                     OGGNFPLQGMHPRANIMRP-RT-NTPKQLRMQLQQRLQGQOFLNQSRQALELKMENPTAG 1201
                                                                                                                                                                                                                                                                                                                                                                                                                    VNLTLRPGV-PTQAPINAQMLAQRQREILNQHLRQ-R-QM--------QQQVQQ 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                  RTLMMRGQGLNVTPSMVAPAGLPAAMSNPRIPQANAQQFPFPPNYGISQQPDPGFTGATT 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PQSPLMSPRMAHTQSPMMQQSQANPAYQPTSDMNGWAQGSMGGNSMFSQQSPPHFGQQAN 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQNRQPFGSSPDDLLCPHPAAESPSDEGALLDQLYLALRNFD--GLEEIDRALGIPELVS 1107
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               FYNNSIS-S-NGS---H--LGT-KQ---Q---VFQ-GTNSLGLKSSQSV-QSIRP----
                                                       LLPNQNLPLDITLQSPTGAGPFPPIRNSSPYSVIPQPGMMG-NQGMLGSQGNLGNNSTGM
                                                                                                                                   SNSIPGARPVLQQQQMLQMRPGEIPMGMGANPYGQA-AASNQLGSWPDGMLSMEQVSHG
                                                                                                                                                                                                                                                                                                RPNYTTLR-MQPRPGLRPTGIVQNQPNQLRLQLQHRLQAQQ--N--RQPL-MNQISSVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQQQQQTQAFSPPPNVTASPSMDGLLAGPTMPQAPPQQFPYQPNYGMGQQPDPAFGRVSS
LFPDTRPGAPTGSVDKQAIINDLMQLTADSSPVPPAGAQKAALRMSQSTFNNPRPGQLGR
                                                                        --PY-N-R-AVSLDSPVSVGSSPPVKNISAFPMLPRQPMLGGNPRAMDSQENYGSSMGGP
                                                                                                                IGSSTSRPSMPSGEWA-PQSPAVRVTCAATTGAMNRPV-Q-G-GMIRNP-TASIP---MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE, 97336097.
TORCHINA J., ROSE D.W., INOSTROZA J., KAMEI Y., WESTIN S., GLASS
ROSENFELD M.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mediates
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   009001;
01-JUL-1997 (TREMBLREL. 04, CREATED)
01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
NUCLEAR RECEPTOR COACTIVATOR 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.3%; Score 2887; DB 11;
40.1%; Pred. No. 0.00e+00;
ative 380; Mismatches 377;
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SEQUENCE 1463 AA; 158880 MW; E367B699 CRC32;
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EMBL; AFO00582; G2213817; -.
MGD; MGI:1276533; NCOA2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1272
                                                                                       1164 PNYTTLR-MOPRPGLRPTGIVQNQPNQLRLQLQHRLQAQQ--N--RQPL-MNQISSVSNV 1217
                                                                                                    :||:::| | :||::|| : |
1085 GQALEPKQDAFQGGEAAVMMDQKAGLYGQTYPAQGPPMGGFHLQGQSPSFNSMMNQMNQ 1144
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ONROPFGSSPDDLLCPHPAAESPSDEGALLDQLYLALRNFD--GLEEIDRALGIPELVSQ
             1025 QNRPLLRNSLDDLVGPPSNLEGQSDERALLDQLHTLLSNTDATGLEEIDRALGIPELVNQ
                                            SQAVDAEQ--FSSQESSIMLEQKPPVFPQQYASQAQMAQGGYN-PMQDPNFHTM-GQ--R
                                                                                                                                    1218 NLTLRPGV-PTQAPINAQMLAQRQREILNQHLRQ-R-QM--------QQQVQQR
                                                                                                                                                                                 1261 TLMMRGQGLNVIPSMVAPAGLPAAMSNPRIPQANAQQFPFPPNYGISQQPDPGFTGATTP
                                                                                                                                                                                              1321 QSPLMSPRMAHTQSPMMQQSQANPAYQPTSDMNGWAQGSMGGNSMFSQQSPPHFGQQANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MMDQKAGLYGQTYPAQGPPMQGGFHLQGQSPSFNSMMNQMNQQGNFPLQGMHPRANIMRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 VKNGPSQNPMMQHPQAASIYQSSEMKGWPSGNLARNSSFSQQQFAHQGNPAVYSMVHMNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPPNVTAPPAWMAXGRTHNATSSSATSFQYP-TPNYGNGDQPTKIQPLGRVSKSSQCNDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-BRAIN;
MEDLINE; 97369492.
MEDLINE; 97369492.
MARGOLIS R.L., ABRAHAM M.R., GATCHELL S.B., LI S.H., KIDWAI A.S.,
BRESCHEL T.S., STINE O.C., CALLAHAN C., MCINNIS M.G., ROSS C.A.;
"CDNAS with long CAG trinuclectide repeats from human brain.";
HUM. GENET. 100:114-122(1997).
EMBL; U80737; G2565050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 326;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 0.00e+00;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Mismatches
                                                                                                                                                                                                                                                                                                                                             326 AA
                                                                                                                                                                                                                                                                         1381 SMYSN-NMNISVSMATNTGGLSSMNQMTGQMSM 1412
                                                                                                                                                                                                                                                                                         1379 AVYSMVHMNGSSGHMGQMN-MNPM-PMSG-MPM 1408
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CATARRHINI; HOMINIDAE; HOMO
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Best Local Similarity 84.1%;
Matches 275; Conservative
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01-JAN-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SGLGDSSSDPANPDSHKRKGSPCDT ---- LASSTEKRRREQENKYLEELAELLSANISDI
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1 Similarity 40.0%; Pred. No. 2.28e-286;
339; Conservative 223; Mismatches 217; Indels 68;
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SEQUENCE FROM N.A.
MEDLINE; 98090466.
MEDLINE; 98090466.
KALKHOVEN E., VALENTINE J.E., HEERY D.M., PARKER M.G.;
"Isoforms of steroid receptor co-activator 1 differ in their it to potentiate transcription by the oestrogen receptor.";
EMBL; A.000802; E1254355; -.
EMBL; A.000802; E1254355; -.
FEMBL; A.000802; E1254355; -.
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ID 043793

AC 043794

AC 043794

AC 043797

AC 04379

AC 043797

AC 04379

AC 0437
SSGHMGQMNMNPMPMSGMPMGPDQKYC 1415
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                             DEKDLRSTPNLSLDDVKVKVEKKEQMDPCNTNPTPMTKPTPE-EIKLEAQSQFTADLDQF 813
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GFYCDQNPVESSMCQSNSRDHLSDKESKESSVEGAENQRGPLESKGHKKLLQLLTCSSDD 631
                                                                                                                    G-SPSDITTLSVEPDKKDSASTSVSVTGQVQGNSSIKLELDASKKKESKDHQLLRYLLDK 754
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larity 40.0%; Pred. No. 2.28e-286;
Conservative 223; Mismatches 217; Indels 68; Gaps
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                                      Q-Q--LRHADIDTSCKDV-LSCTGTSNSASANSSGGSCPSS-HSSL-TERHKILHRLLQE
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LAST ANNOTATION UPDATE)
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SEQUENCE 1440 AA; 156624 MW; B8374AC7 CRC32;
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EURARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
                                                              641
                                                                                                                                                                                                                                                                                                       DEKDLRSTPNLSLDDVKVKVEKKEQMDPCNTNPTPMTKPTPE-EIKLEAQSQFTADLDQF 813
LQMPSSRAY-GLA-DPSTTGQMSGARYGGS-S-NIAS-LTPGPGM-QSPSSYQNNNYGLN 462
                                                                                                                                                                                                                                                                                                                                                                 G-SPSDITTLSVEPDKKDSASTSVSVTGQVQGNSSIKLELDASKKKESKDHQLLRYLLDK 754
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MEDLINE; 96291002.
TARESHITA S., YEN P.M., MISITI S., CARDONA G.R., LIU Y., CHIN W.W.;
Molecular cloning and properties of a full-length putative thyroid
hormone receptor coactivator.";
ENDOCRINOLOGY 1373594-3597(1996).
                                                                                                                     RSYSNIPVTSLQGMNEGPNNSVGFSASSPVLRQMSSQNSPSRLNI-QPAKAESKDNKEIA
                                                                                                                                          LNNSPMEGTGISLAQFMSPRRQVTSGLATRPRMPNNSFPPNISTLSSPVGMTSSACNNNN
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                                                                                                                                                                                                                                                                                  642 Q-Q--LRHADIDTSCKDV-LSCTGTSNSASANSSGGSCPSS-HSSL-TERHKILHRLLQE
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LAST ANNOTATION UPDATE)
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P -> S (IN REF. 2).
A -> E (IN REF. 2).
A -> E (IN REF. 2).
T -> N (IN REF. 2).
T -> M (IN REF. 2).
MISSING (IN REF. 2).
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Pred. No. 2.08e-285;
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IISSUE-CARDIAC, AND SKELETAL MUSCLE;
SPENCER T.E., JENSTER G., ONATE S., TSAI M.J.,
SUBMITTED (MAR-1997) TO EMBL/GENBANK/DDBJ DATA
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Somilarity 39.9%;
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P70366 PRELIMINARY; PRT; 1405 AA.
01-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
NUCLEAR RECEPTOR COACTIVATOR 1 (STEROID RECEPTOR COACTIVATOR-1).
NCOAL OR MSRC-1.
MUS MUSCULUS (MOUSE).
EUKARYOTA: METAZOA: CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; RODENTIA;
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PROC. NATL. ACAD. SCI. U.S.A. 93:10626-10631(1996)
EMBL; U64828; G1490876; --
MGD; MGI.1276523; NCOAI.
PFAM; PF00989; PAS; 1.
SEQUENCE 1405 AA; 152643 MW; 1743F755 CRC32;
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SCIUROGNATHI; MURIDAE; MURINAE; MUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLEALDGFFFVVNCEGRIVFVSENVTSYLGYNQEELMNTSVYSILHVGDHAEFVKNLLPK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSGLGDSSSDPANPDSHKRKGSPCDT----LASSTEKRRREQENKYLEGLAELLSANISD 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        470 LNLNNSPMEGTGIALSQFMSPRRQANSGLATRARMSNNSFPPNIPTLSSPVGITSGACNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVRKCIYAFFQPQGREPSYARQLFQEVMTRGTASSPSYRFILNDGTMLSAHTKCKL-CYP
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                                                            01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLEREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLEEL. 08, LAST SHOTATION UPDATE)
NUCLEAR RECEPTOR COACTIVATOR 1 (STEROID RECEPTOR COACTIVATOR 1A)
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                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

KAMEI Y., XU L., HEINZEL T., TORCHIA J., KUROKAWA R., GLOSS
LIN S.C., HEYMAN R.A., ROSE D.W., GLASS C.K., ROSENFELD M.G.
CELL 0:0-0(0)

EMBL; U56920; G1336160; -.

MGD; MGI:1276523; NCOAI.
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Pred. No. 2.05e-280;
229; Mismatches 215;
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                    1405
                      PRT;
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                      PRELIMINARY;
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                                                                                                                                                       OR SRC1A.
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JT 11
Q61202
Q61202;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 LLEALDGFFFVVNCEGRIVFVSENVTSYLGYNQEELMNTSVYSILHVGDHAEFVKNLLPK 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSGLGDSSSDPANPDSHKRKGSPCDT----LASSTEKRRREQENKYLEELAELLSANISD 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 QGDGEDFQSCLICIARRLPRP-PAI-TGVESFMTKQDTTGKIISIDTSSLRAAGRTGWED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ::|:|| || :: ::|| || || 296 IIRRCIQRFFSLNDGQSWSQKRHYQEAYLNGHAETPVYRFSLADGTIVTAQTKSKLFRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 LVRKCIYAFFQPQGREPSYARQLFQEVMTRGTASSPSYRFILNDGTMLSAHTKCKL-CYP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              470 LNLNNSPMEGTGIALSQFMSPRRQANSCLATRARMSNNSFPPNIPTLSSPVGITSGACNN
                     YLLDKDEKOLRSTPNLCLDDVKVKVEKKEQMDPCNTNPTPMTKPAPE-EVKLESQSQFTA
                                                                                                        LOEG-SPSDITTLSVEPEKKDSVPASTAVSVSGQSQGSASIKLELDAAKKKESKDHQLLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
SCIUROGNATHI; MURIDAE; MURINAE; MUS.
                                                                                                                                                                                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 16.7%; Score 1642; DB 11;
Best Local Similarity 39.4%; Pred. No. 5.31e-276;
Matches 336; Conservative 231; Mismatches 215;
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                                                                                                                                                                                                                                                                                      1447
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01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
STEROID RECEPTOR COACTIVATOR.
HOMO SAPIENS (HUMAN).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1013 GMLSWEQVSHGTQNRPLLRNSLDDLVGPPSNLEGQSDERALLDQLHTLLSNTDATGLEEI 1072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          757 YLLDKDEKDLRSTPNLCLDDVKVKVEKKEQMDPCNTNPTPMTKPAPE-EVKLESQSGFTA 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HONROAI-LNOFAATAPVGINMRSGMOQOITPQPPLNAQMLAQRQRELYSQQHRQ-R-QL 746
                                                                                                                                     : :: : | | | :: | | :| | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                            586 SKEIASILNEMIQSDNSDN-SANEGKPLDSGLLHNNDRLSEGDSKYSQTSHKLVQLLT-T
                                                                                                                                                                                                                                                                                                                                                                                                    | :| ||::::::::||| ::||| ||: || ||: ||| ||: |||| ||: |||| ||!||| LQNGNSPAEVAKITAQATGKDT--SSIT-S-CGD--GNV-VKQEQLSPKKKE--NNALLR
514 NTVTAINQSK-SEDQCI-SSQLDELLCPPTTVEGRNDEKALLEQLVSFLSGKDETELAEL
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ONATE S.A., TSAI S.Y., TSAI M.J.;
Sequence and characterization of a coactivator for the steroid hormone receptor superfamily.";
SCIENCE 270:1354-1357(1995).
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Pred. No. 1.07e-87;
89; Mismatches 89; Indels 2
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O'MALLEY B.W., ONATE S.A., TSAI S.Y., TSAI M.J.;
SUBMITIED (NOV-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL: U40396; G1117915; -..
SEQUENCE 1061 AA; 114166 MW; 65252254 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1061 AA
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Local Similarity 36.2%;
les 113; Conservative
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796 DLDNLDAILGDL 807
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HOMO SAPIENS (HUMAN).
EUKARYOTA; META2OA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
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EUKARXOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA; PRIMATES;
CATARRHINI; HOMINIDAE; HOMO.
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Best Local Similarity 33.9%; Pred. No. 3.35e-22;
Matches 81; Conservative 46; Mismatches 91; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 416;
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SUBMITTED (MAR-1998) TO EMBL/GENBANK/DDBJ DATA BANKS.
EMBL; AF056191; G3037135; -.
SEQUENCE 579 AA; 63879 MW; BAD0C268 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BANKS
                                                                                                                                                                                                      01, CREATED)
01, LAST SEQUENCE UPDATE)
07, LAST ANNOTATION UPDATE)
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01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE)
01-AUG-1998 (TREMBLREL. 07, LAST ANNOTATION UPDATE)
TPA INDUCTBLE PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
RAINERI I., SOLER M., SENN H.;
SUBMITTED (DEC.1994) TO EMBL/GENBANK/DDBJ DATA I
EMBI, U19179; G726038; -.
SEQUENCE 416 AA; 45239 MW; F6F46600 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.8%; Score 376; DB 4; 1
12.1%; Pred. No. 2.68e-40;
1tive 39; Mismatches 40
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Conservative
                                                                                                                                                 PRELIMINARY;
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01-NOV-1996 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
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1242 MMQQQQQQQQQQ 1253
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nes 67; Conser
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ID 060657
AC 060657;
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AC Q13071;
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Search completed: Fri Sep 17 21:16:25 1999 Job time : 245 secs.

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1 GCTGGATGGACTCAGAG.........CATTTGAGCAGGAATTCTAG 4496
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Sequence 1,
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Sequence 5,
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/cgn2_6/ptodata/1/lna/5B_COMB.seq:*
/cgn2_6/ptodata/1/lna/5C_COMB.seq:*
/cgn2_6/ptodata/1/lna/FOTOSB.seq:*
/cgn2_6/ptodata/1/lna/PCTUS9_COMB.seq:*
/cgn2_6/ptodata/1/lna/PCTUS9_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
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US-08-002-999-3
US-08-816-693A-1
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38	GACAACAGAGGGTGGCTATC	AAGTCATCACTTCC		
3; Length 195; 1; 43; Indels 0; Gaps	; Score 73.2; DB 3; ; Pred. No. 1.7e-11; 0; Mismatches 43	1.6%; Similarity 69.7%; 9; Conservative	Match Jocal Simi es 99;	Query Best 1 Match
		SS: single linear E: DNA	DEDN OGY: E TY	80-SD
	2:	ILELEHANE: 012-305-1215 TELEFAX: 612-305-1215 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 195 base pairs TYPE: nucleic acid	TELEFACIE: TELEFAX: FORMATION FOI SEQUENCE CHAL LENGTH: 10	N
	ON: 33,977 R: 110.00030101 PATION:	CLASSILATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Mueting, Ann M. REGISTRATION NUMBER: 33,977 REFERENCE/DOCKET NUMBER: 11 TELECOMMUNICATION INFORMATION:	CLASSIFICATION: ATTORNEY/AGENT INFORM NAME: MUETING, AND REGISTRATION NUMBER REFERENCE/DOCKET NU TELECOMMUNICATION INF	
1.25	Compatible PC-DOS/MS-DOS IIN Release #1.0, Version #1 A DATA: OVERSION #1 UN 1995	IBM PC compatibl SYSTEM: PC-DOS/M Patentin Release ICATION DATA: N NUMBER: US/08/ E: 06-JUN-1995	COMPUTER: IBM PC COMP OPERATING SYSTEM: PC- SOFTWARE: PATENTIN RE CURRENT APPLICATION DATA APPLICATION NUMBER: U FILING DATE: 06-JUN-1	
		SA ABLE F	STATE: MN COUNTRY: US ZIP: 55401 COMPUTER READS	
Diagnosis Schwappach, P.A. , Suite 203	d Method for Gebhardt & ourth Street	pe 7 Raa 645	TITLE OF INVENTION: TY NUMBER OF SEQUENCE: 4 CORRESPONDENCE ANDRESS: ANDRESSE: Mueting, STREET: 119 No. 5741 CITY: Minneapolis	
Spinocerebellar Ataxia	469802B .W. Sequence for	US/08 'Y T. 'ura P. ng-yi luda Y	S E CC LC LC .	US-08-469 Sequenc Patent GENERA APPL APPL APPL APPL APPL APPL TITL Patent
	ALIGNMENTS			
Sequence 1, Appli Sequence 7, Appli	US-08-472-478-1 US-08-463-081B-7 US-08-461-379A-7 US-08-461-379A-7 US-08-461-379A-7 US-08-462-390B-7 US-08-462-390B-7 PS-08-462-390B-7 PS-08-462-390B-30	1.2 2946 4 1.2 2946 4 1.2 2289 4 1.2 2289 4 1.2 2289 4 1.2 2289 4 1.2 2289 4 1.2 2289 4	52.8 52.8 52.8 52.8 52.8 52.8 52.8 52.8	Μ Μ ব ব ব ব ব ব

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ATTORNEY AGENT INFORMATION:
NAME: Mucting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCET NUMBER: 110.00030101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1227
INFORMATION FOR SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 168 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/08469802B; Patent No. 5741645; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3888 CCCAGGCCTTCAGCCCACCTCC 3909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 69.7
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                    STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-469-802B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-469-802B-4
                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
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APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Chung, Ming-yi
APPLICANT: Colpbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSE: Mueting, Rasach, Gebhardt & Schwappach, P.A.
STREET: 119 No. 5741645th Fourth Street, Suite 203
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.6%; Score 73.2; DB 3; Length 234; Best Local Similarity 69.7%; Pred. No. 1.9e-11; Matches 99; Conservative 0; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: MUCLING, AND M.
REGISTRATION NUMBER: 33,977
REBERNCE/DOCKET NUMBER: 33,977
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                     Sequence 3, Application US/08469802B
Patent No. 5741645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08469802B
Patent No. 5741645
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164 AGCAGCACCTCAGCAGGGCTCC 185
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 234 base pairs TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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APPLICANT: Orr, He
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3768 AGCTGCTAAGTCATCACTTCCGACAACAGGGGTGGCTATGATGATGCAGCAGCAGCAAC 3827
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APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-Yi
APPLICANT: Coghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 47
APPLICANT: Chung, Ming-yi
APPLICANT: Coghbi, Huda Y.
TILE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                    P.A.
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Minneapolis
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                                                                                                                                                                                 ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, STREET: 119 No. 5741645th Fourth Street, Suite 203 CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
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69.7%; Pred. No. 1.5e-11;
tive 0; Mismatches 43;
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TOPOLOGY:
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APPLICANT: Parry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Codhbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
PATILE OF INVENTION: Type 1 and Method for Diagnosis
TITLE OF SEQUENCES: 85
CORRESPONDENCE: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STRRET: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3; Length 171;
                                                                                                           SOFTWARENT PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTONINY/AGENT INFORMATION:
NAME: MUELING, ANN M. NAME: MUELING, ANN M. REGISTRENCE/DOCKET NUMBER: 110.00030101
TELEPROMUNICATION INFORMATION:
TELEPROMUS: 612-305-1225
TELEPRAKEN: 612-305-1225
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
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69.7%; Pred. No. 1.6e-11;
tive 0; Mismatches 43
                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 69.79
Matches 99; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 171 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA
USA
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US-08-267-803B-2
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3768 AGCTGCTAAGTCATCACTTCCGACAACAGGGGTGGCTATGATGATGCAGCAGCAGCAGC 3827
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APPLICANT: Orr, Harry T.
APPLICANT: Chung, Ming-yi.
APPLICANT: Chung, Ming-yi.
APPLICANT: Coghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 73.2; DB 4; Length 195; Pred. No. 1.7e-11;
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P.O. Box 581415
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCOTMACK, MYTA H.
REGISTRATION NUMBER: 36,602
REGISTRATION NUMBER: 36,602
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELEPOMUNICATION INFORMATION:
TELEPOMORE: 612-305-1217
TELEPOMORE: 612-305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Patent No. 5834183
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COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3888 CCCAGGCCTTCAGCCCACCTCC 3909
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                                                                                                                                                                                                                                 LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 69.77
Matches 99; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Orr, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Cognbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS: 85
CORRESPONDENCE ADDRESS: 85
                                                                                                                                                                                                Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
                                                                                                                                                                                                                                             43; Indels
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ZIP: 55458-1415

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCOFMEACK, MYTE H.
REGISTRATION NUMBER: 36,602
REFERENCE/COCKET NUMBER: 310.00030120
TELEPHONE: 612-305-1217
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1228
INPORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 108 base pairs
TYPE: NUCLEIC acid
STRANDEDBESS: single
                                                                                                                                                                                              Query Match 1.6%; Score 73.2; DB 4;
Best Local Similarity 69.7%; Pred. No. 1.9e-11;
Matches 99; Conservative 0; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08267803B Patent No. 5834183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 AGCAGCACCTCAGCAGGCTCC 224
SEQUENCE CHARACTERISTICS:
LENGTH: 234 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
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                                                                                                                                US-08-267-803B-3
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STATE:
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Length 168;

DB 4;

Score 73.2;

1.68;

Query-Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
STAIE: MN
                     Indels
                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08267803B
Fatent No. 5834183
GENERAL INFORMATION
APPLICANT: Ranum, Laura P.W.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Ranum, Laura P.W.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar;
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USAR

2 | 19: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCORMACK, Myra H
REFERENCE/DOCKET NUMBER: 110.00030120
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ ID NO: 5:
Best Local Similarity 69.7%; Pred. No. 1.5e-11;
Matches 99; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                 3888 CCCAGGCCTTCAGCCCACCTCC 3909
                                                                                                                                                                                                                                                                  137 AGCAGCACCTCAGCAGGCTCC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 171 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 69.77
Matches 99; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: DNA
US-08-267-803B-5
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US-08-267-803B-5
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STRANDEDNESS:
TOPOLOGY: lin
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                                                                                                                                                                                  APPLICANT: Orr, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Coung, Ming-yi
APPLICANT: Zoghbi, Huda yi
APPLICANT: Soghbi, Huda yi
APPLICANT: TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5/41645
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 3366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 68.4; DB 3; Length 33
Pred. No. 2.1e-09;
0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: BEN PC COMPATIBLE

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,802B

FILING DATE: 06-JUN-1995

FILING DATE: ....ATION:
                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Mueting, Reasch, Gebhardt & Schwappach, STREET: 119 No. 5741645th Fourth Street, Suite 203 CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3880 GCAGCAAACCCAGGCCTTCAGCCCACCTCC 3909
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; Sequence 6, Application US/08469802B
; Patent No. 5741645
                                                                                                                                Sequence 1, Application US/08469802B
Patent No. 5741645
                                  140 AGCAGCACCTCAGCAGGGCTCC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 11.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225
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LENGTH: 3366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 66.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                            US-08-469-802B-1
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3767 GAGCTGCTAAGTCATCACTTCCGACAACAGGGGTGGCTATGATGATGCAGCAGCAGCAA 3826
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APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
FITLE OF INVENTION: Type I and Method for Diagnosis
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Meting, Raasch, Gebhardt & Schwappach, P.A.
ADDRESSEE: Meting, Raasch, Gebhardt & Schwappach, P.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/08469802B
Patent No. 5741645
GENERAL INFORMATION:
APPLICANT: Orr, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Chung, Ming-yi
TITLE OF INVENTON: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5741645
                                                                                                                                                       ADDRESSEE: Mueting, Reasch, Gebhardt & Schwappach, STREET: 119 No. 5741645th Fourth Street, Suite 203 CITY: Mineapolis STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 612-305-1217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 1.5%;
Best Local Similarity 71.4%;
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
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US-08-267-803B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 CAACATGGGCAGTCTGAGCCAGACGCCGGGACACAAGGCTGAGCAGCAGCAGCAGCAGCA
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Patent No. 5834183
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-y1
APPLICANT: 209hbi, Huda Y.
ITILE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.5%; Score 68.4; DB 3; Length 506; Best Local Similarity 66.0%; Pred. No. 6.7e-10; Matches 99; Conservative 0; Mismatches 51; Indels
ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: 119 No. 5741645th Fourth Street, Suite 203
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415
CITY: Minneapolis
                                                                                                                                                               E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-UNA-1995
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 110.00030101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 506 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3880 GCAGCAAACCCAGGCCTTCAGCCCACCTCC 3909
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA
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3760 CAGCAGAGAGCTGCTAAGTCATCACTTCCGACAACAGAGGGTGGCTATGATGATGCAGCA 3819
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                                                                                                                                                                                                                                                                                                                                            Query Match 1.5%; Score 68.4; DB 4;
Best Local Similarity 66.0%; Pred. No. 2.1e-09;
Matches 99; Conservative 0; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1836 GCAGCAGCAGCACCTCAGCAGGGCTCC 1865
                                                                                                                           110.00030120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3880 GCAGCAAACCCAGGCCTTCAGCCCACCTCC 3909
SOFTWARE: Patentin Release #1.0, ve CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B FILING DATE: 28-JUN-1994
                                                        CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: MCCLTMACK, MYDA H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-127
TELEPHONE: 612-305-127
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3366 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: single
TYPE: NUCLEIC acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCOrmack, Myra H.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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US-08-267-803B-6
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Gaps

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Length 506;

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Score 68.4; DB 4; Length 5(
Pred. No. 6.7e-10;
0; Mismatches 51; Indels
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                                      Query Match 1.5%;
Best Local Similarity 66.0%;
Matches 99; Conservative
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TELEPAX: 612-305-1228
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 10660 base pairs
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Best Local Similarity 66.0°
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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936..3384
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MOLECULE TYPE:
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; LOCATION:
US-08-267-803B-8
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APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi.
APPLICANT: Chung, Ming-yi.
APPLICANT: Chung, Ming-yi.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
FITLE OF INVENTION: Type 1 and Method for Diagnosis
UNMER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. BOX 581415
CITY: Minneapolis
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                                                                                                                                                                                                                              Score 68.4; DB 4; Length 154;
Pred. No. 3.3e-10;
0; Mismatches 36; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
CLASSIFICATION: 435
ATONEY/AGENT TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: MCCOTMACK, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFRONE: 612-305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08267803B
Patent No. 5834183
GENERAL INFORMATION:
APPLICANT: OTT, Harry T.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                              Query Match 1.5%;
Best Local Similarity 71.4%;
Matches 90; Conservative
612-305-1217
                TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 base pairs
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STRANDEDNESS: single
                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                              ; TOPOLOGY: linear; MOLECULE TYPE: DNA US-08-267-803B-6
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                                               Gaps
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APPLICANT: Sanum, Laura P. W.
APPLICANT: Chung, Ming-4,
APPLICANT: Coghbi, Huda Y.
TILE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
Patent No. 5834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
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COUNTRY: USA

ZIP: 55458-1415

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
OPERATION SYSTEM: PC-DOS/MS-DOS
CORTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-JUN-1994
FILING DATE: 28-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, STREET: P.O. Box 581415
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Pred. No. 4.2e-09;
0; Mismatches 51;
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                                                                                                                                                                                                                                         225 GCAGCACCAGCACCTCAGCAGGGCTCC 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MCCORMACK, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEPHONE: 612-305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    õ
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Search completed: September 18, 1999, 01:49:11 Job time: 18403 sec

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Compugen Ltd.
GenCore version 4.5
Copyright (c) 1993 - 1998 Comp
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- nucleic search, using sw model OM nucleic

September 17, 1999, 20:44:41; Search time 152.06 Seconds (without alignments) 7397.498 Million cell updates/sec Run on:

US-09-041-994-1 Title:

4496 1 GCTGGATGGTGGACTCAGAG......CATTTGAGCAGGAATTCTAG 4496 Perfect score: Sequence:

IDENTITY_NUC Scoring table: 311585 segs, 125096042 residues Searched:

N_Geneseq_36:* tabase :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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TGGTGAAAAACGGAGCGGGAGCAGGAAAGTAAATATTGAAGAATTGGCTGAGCTGAT

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ò පු ò g 241 ATCTGCCAATCTTAGTGATATTGACAATTTCAATGTCAAACCAGATAAATGTGCGATTTT 300

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New isolated steroid receptor co-activator, AIB1 - used to develop products for the diagnosis and treatment of steroid-responsive unouses, e.g. breast, lung, prostate or colon cancers or melanomas Claim 7; Page 25-30; 57pp; English.

The AIB1 protein is a member of the steroid receptor coactivator-1 (SCR-1) family of nuclear receptor co-activators that interact with estrogen receptors (ER) to enhance ER-dependent transcription.

The AIB1 polypeptide can be used to identify compounds which inhibit endicates aberrantly proliferating cells, thus detection of indicates aberrantly proliferating cells, thus detection of indicates aberrantly proliferating cells, thus detection of indicates aberrantly proliferating cells, thus detection of predisposition towards developing cancer. Compounds which inhibit composition of AIB1 on compounds which inhibit interaction of AIB1 or compounds which inhibit with steroid receptors or nuclear co-factors can be used for reducing the proliferation of cancer cells.

Sequence 6835 BP; 1988 A; 1479 C; 1528 G; 1840 T;
SCA2 gene CAG repe
SCA2 gene fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AGCCAGITGCTGATGTATICAAGATGAGTGGATTAGGAGAAAACTTGGATCCACTGGC 120
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                                                                                                                                                                                                     AIB1 (Amplified in breat cancer-1) gene.

AIB1 (Amplified in breast cancer; steroid; receptor;

AIB1; amplified in breast cancer; cancer; steroid; receptor;

Coactivator; SCR; estrogen; ER; estrogen dependent transcription;

breast cancer; lung cancer; colon cancer; prostate cancer;

melanoma; ss.

Location/Qualifiers

CDS

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99.5%; Pred. No. 0;
iive 0; Mismatches
                                                                       ALIGNMENTS
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/product= AIBl_protein
V17233
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V99915;
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17-JUN-1998; U12689.
17-JUN-1997; US-049728.
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Meltzer P, Trent JM;
WPI; 99-080946/07.
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rgcga	TTCCA	3=3	8 = 8	AGAGG AGAGG	858	ACAAA 	AGACA AGACA	片드片	SGCAC 11-11 SGCAC	CAGAC	SAGGC SAGGC		AGAAACCCC	CAAAC	TCAGAGAGA 	CACCTA!	TACAGP TACAGP	rggagg rggagg
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CAATT	CAAAT	H-H	ATTGG 	GTCA	CTTAC	⊢ − ⊢	GATGA GATGA	TATG	GATGGAGGAAGGGAAGATTTGCAAT(TACTACAGGAGAAAGAACATTTCCAT 	GATA 	GTATIC GTATIC	CAAGAAGC	SGAACTATAGTGACTG 	GACATGGC	CAAATCCTC	CATGAGTP CATGAGTP	CAGACCCTAGCACCACAGGCCAGATI
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356	301	36]	421 536	481 596	54]	603	661	721	781	841 95(901	961	1023	108]	1143	1203	1261	132
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TTCCTACCAGAACAACAACTATGGGCTCAACATGAGTAGCCCCCCCACATGGGAGTCCTGG TCTTGCCCCAAAACCAGGAATATCATGATTTCTCCTCGTAATGGTGGAGGTCCAAAGAT 2456 TAAAGAACTACAGCCCCAAGTGGAAGGAGTGGATAATAAAATGAGTCAGTGCACCAGCTC TACTGGGAACCACACCTTTTCCAGCAGCTCTCTCAGTGCCCTGCAAGCCATCAGTGAAGG TGTGGGGACTTCCCTTTTATCTACTCTGTCATCACCAGGCCCCAAATTGGATAACTCTCC CAATATGAATATTACCCAACCAAGTAAAGTAAGCAATCAGGATTCCAAGAGTCCTCGGG GGGTCATTCCTCCTTGACCAACTCCCCCTAGATTCAAGTTGTAAAGAATCTTCTGTTAG TATGCATGGGTCACTGTTACAAGAAGCACCGGATTTTTGCACAAGTTGCTGCAGAATGG GAATTCACCAGCTGAGGTAGCCAAGATTACTGCACAAGCCACTGGGAAAGACACCAGCAG TAAAGAACTACAGCCCCAAGTGGAAGGAGTGGACAATAAAATGAGTCAGTGCACCAGCTC CACCATTCCTAGCTCAAGTCAAGAGAAGACCCTAAAATTAAGACAGAGACAAGTGAAGA TCTTGCCCCAAACCAGCAGAATATCATGATTTCTCCTCGTAATCGTGGGAGTCCAAAGAT AGCCTCACATCAGTTTTCTCCTGTTGCAGGTGTGCACTCTCCCCATGGCATCTTCTGGCAA g g 임 P Q g g g 셤 유 요 8 g 8 8 ò 8 8 8 8 O D ò δ à 셤 ò ģ ç ò δ ò ö

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12;
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The AIB1 protein is a member of the steroid receptor coactivator-1 (SCR-1) family of nuclear receptor co-activators that interact with estrogen receptors (ER) to enhance ER-dependent transcription.

The AIB1 polypeptide can be used to identify compounds which inhibit ER-dependent transcription. Increased expression of the AIB1 gene an be used to identify compounds which inhibit ER-dependent transcription. Increased expression of the AIB1 gene can be used to diagnose cancer or a copies of the AIB1 gene can be used to diagnose cancer or a predisposition towards developing cancer. Compounds which inhibit expression of AIB1 or compounds which inhibit interaction of AIB1 catedual receptors or nuclear co-factors can be used for reducing the proliferation of cancer cells. This sequence is of the murine pCIP gene, a mouse ortholog of AIB1.

Sequence 4621 BP; 1227 A; 1244 C; 1194 G; 956 T;
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AIB1; amplified in breast cancer; steroid; receptor; coctivator; SCR; estrogen; ER; estrogen dependent transcription; breast cancer; lung cancer; colon cancer; prostate cancer; melanoma; ss.
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Best Local Similarity 79.7%; Pred. No. 0;
Matches 3547; Conservative 0; Mismatches
                                                                                                                                          /*tag= a
/product= pCIP_protein
                                                                                                         Location/Qualiflers
110. .4453
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(USGO ) US GOVERNMENT.
Meltzer P, Trent JM;
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17-JUN-1997; US-049
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8 IGGICIIGGICCCAACCAGCAGAACAICAIGAITICCCCICGGAAICGIGGCAGCCCAAA	8 GAIAGCCICACAICAGITITICICCIGIIGCAGGIGIGCACICICCCCAIGGCAICITICIGG	3 CAATACTGGGAACCACCACTGCAGCGCTCTCTCAGTGCCCTGCAAGCCATCAGTGA	8 AGGIGIGGGACITCCTITIAICIACITCIGICAICACCAGGCCCCAAAIIGGAIAACIC 	3 TCCCAATAIGAATATTACCCAACCAAGTAAAGTAAGCAATCAGGATTCCAAGAGTCCTCT	3 GGGCTTTTATTGCGACCAAAATCCAGTGGAGAGTTCAATGTGTCAGTCA	3 TCACCTCAGTGACAAAGAAAGTAAGGAGAGCAGTGTTGAGGGGGCAGAGAATCAAAGGGG	3 TCCTITGGAAAGCAAAGGTCATAAAAATTACTGCAGTTACCTGCTGCTGCTGTGTGTG	CCGGGGTCATTCCTCCTTGACCAACTCCCCCTGGATTCAAGTTGTAAGAATCTTCTGT	3 TAGTGTCACCAGCCCTCTGGAGTCTCCTCCTACATCTGGAGGAGTATCCTCTACATC	3 CAATAIGCAIGGGTCACTGTIACAAGAGAAGCACCGGATTIITGCACAAGTIGCIGCAGAA 	3 TGGGAATTCACCAGCTGAGGTAGCCAAGATTACTGCACAAGCCACTGGGAAAGACACGGGAAGACACGGGAAGACACGGGAAGACACGGGAAGACACGAGGAACTCCCCAGCGGAAGGACGCCAAGATCACTGCAAGAGCCACTGGGAAGGACACGAG	3 CAGTATAACTICTIGIGGGGACGGAAAIGTIGICAAGCAGGAGCAGCAAAGICCIAAGAA	B GAAGGAGAATAATGCACTTCTTAGATACCTGCTGGACAGGGATGATCCTAGTGATGCACT	8 CICTARAGAACTACAGCCCCAAGIGGAAGGAGGACAGAGAATAAAATGAGICAGIGGACCAG 	8 CTCCACCATTCCTAGCTCAAGTCAAGAGACCCTAAAATTAAGACAGAGACAAGTGA 	8 AGAGGGATCTGGAGACTTGGATAATCTAGATGCTATTCTTGGTGATCTGACTAGTTCTGA	8 CITITACAAFAATTCCATAICCTCAAATGGTAGTCATCTGGGGACTAAGCAACAGGTGTT	TCAAGGAACTAATTCTCTGGGTTTGAAAGTTCACAGTCTGTGCAGTCTATTCGTCCTCC
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p/CIP gene.
p/CIP; p300/CBP/co-integrator-associated protein; gene expression; cancer; inflammatory disease; atherosclerosis; osteoporosis; ds.
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WPI: 99-080883/07.
P-PSDB; W99481.
New nucleic acids encoding p/CIP and NcoA-2 polypeptides - are used to identify agents that regulate gene expression, e.g. for treatment of cancer, inflammatory disease and osteoporosis
                                                                         3760 CATGATG-----CCCCAGGCTTTCTTTAATGCCCAAATGGCTGCCCAGCAGAACGAGA
                                                                                                                                                                                                                         GCTGCTAAGTCATCACTTCCGACAACAGAGGGTGGCTATGATGATGCAGCAGCAACA
                                                                                                                                                                                -----GTCACAACCACAGCC
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ACAGGCACTTGAATTGAAAATGGAAAACCCTACTGCTGGTGGTGGTGGTGGTGATGAGGCC
                        3706 GCAGGCACTTGAAATGAAAATGGAGAACC----CTGCTGGCACTGCTGATGAGGCC
                                                  TATGATGCAGCCCCAGCAGGGTTTTCTTAATGCTCAAATGGTCGCCCAACGCAGAGA
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X26000;
08-JUN-1999 (first entry)
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W09856806-Al.
17-DEC-1998. U12263.
12-UNV-1997; US-049452.
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Claim 3; Fig 1; 100pp; English.

This sequence represents the nucleic acid encoding the mouse p/CIP
(p300/CBP/co-integrator-associated protein) polypeptide. The protein
can regulate gene expression so are potentially useful therapeutically,
eg. against (breast) cancer, inflammatory disease (e.g. atherosclerosis)
or osteoporosis.
Sequence 4860 BP; 1274 A; 1302 C; 1251 G; 1031 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GTCAGTTGCTGATCTGTGATCAGGATGAGTGGACTAGGCGAAAGCTCTTTGGATCGCT 144
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ATGCTTCAAATGAGGCCTGGTGAAATCCCCATGGGAA 3062 || | GGGA---CAACCAGGCAGGAGCAGCTGAGAGA TIGGAAGTCCACAGCCTGTGCAGTCTGTTCGTCCTC GGAAATGTTGTCAAGCAGGAGCAGCTAAGTCCTAAGA AGATACCTGCTGGACAGGGATGATCCTAGTGATGCAC GTGGAAGGAGTGGACAATAAAATGAGTCAGTGCACCA ITGAAAAGTICACAGICIGIGCAGICIATICGICCIC GATAGCCCTGTTTCTGTTGGCTCAAGTCCTCCAGTAA TTACCAAAGCAACCCATGTTGGGTGGGAATCCAAGAA GGCTCAAGTATGGGTGGGCCAAACCGAAATGTGACTG GACTGGGGCTTACCAAACTCAAAGGCCGGCAGAATGG GGAAGACCAGGAGGAGATTATAATACTTCTTTACCCA CAGCAGCAACAGCAACAGCAACAACAGCAGC GCCAAGATTACTGCACAAGCCACTGGGAAAGACACCA

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New isolated transcriptional intermediary factor-2 - useful in assays for drugs which are capable of enhancing or inhibiting anculear receptor-mediated pathways

Tuclear receptor-mediated pathways

Claim 1; Fig 1A·B; 119pp; Boglish.

This cDNA clone codes for a novel nuclear receptor transcriptional mediator (see W47532) designated transcriptional intermediary factor-2 (TIF2).

This cDNA clone codes for a novel nuclear receptor transcriptional intermediary factor-2 (TIF2).

This cDNA clone codes for a novel nuclear receptor in the ligand binding domains (LBD) of several nuclear receptors (NR) in an agonist- and entended of the series of t
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12-JUL-1996; US-OJ1247.
(BRIM ) BRISTOL-WIERS SQUIBB CO.
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(INRM ) INST NAT SANTE & RECH MEDICALE.
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Chambon P, Gronemeyer H, Lutz Y, Voegel J; WPI; 98-110525/10.
P-PSDB; W42632.
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20-JUL-1998 (first entry)
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                        Indels 276;
 Length 6156
Score 561; DB 1; I
Pred. No. 7.4e-142;
0; Mismatches 1835;
Query Match 12.5%;
Best Local Similarity 51.0%;
Matches 2198; Conservative
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2544 2937 3111 C---TGGCCCGATGCCATGTTCCATGGAACAAGTTTCTCATGGCACTCAAAATAGGCC 3168 TCCTAAGAAGAAGAGAATAATGCACTTCTTAGATACCTGCTGGACAGGGATGATCCTAG TCCTGCCAGTAACACAAAATTAATAGCAATGAAAACTGAGAAGGAGGAGATGAGCTTTGA TAGIICIGACITITACAATAATICCATATCC ------------------TCAAA GAATAGTCAATTACCACAGGTTTTCCCAGACGAGGCCAGGCGCCCCTGCTGGATCAGT 2904 ACCTCAGCCAGGAATGATGGGTAATCAAGGGATGATAGGAAACCAAGGAAATTTAGGGAA 2964 CAGTAGCACAGGAATGATTGGTAACAGTGCTTCTCGGCCTACTATGCCATCTGGAGAATG ----GCGAGACCAGTATTGCAACAGCAGCAGCAGGTGCTTCAAATGAGGCCTGGTGAAAT TGGGAATTCACCAGCTGAGGTAGCCAAGATTACTGCACAAGCCACTGGGAAAGACACCAG CAGCAGTTCCCCTGTGGACTTGGCCAAGTTAACAGCAGAAGCCACAGGCAAAGACCTGAG CCAGGAGTCCAGCAGCACAGCTCCTGGATCAGAAGTGACTATTAAACAAGAGCCGGTGAG TGAIGCACTCTCTAAAGAACTACAGCCCCAAGIGGAAGGAGTGGACAATAAAATGAGTCA GACAAGTGAAGAGGGATCTGGAGACTTGGATAATCTAGATGCTATTCTTGGTGATCTGAC TGGTAGTCATCTGGGGACTAAGCAACAGGTGTTTCAAGGAACTAATTCTGGGGTTTGAA AAGTTCACAGTCTGTGCAGTCTATTCGTCCTCCATATAACCGAGCAGTGTCTCTGGATAG CCCTGTTTCTGTTGGCTCAAGTCCTCCAGTAAAAATATCAGTGCTTTCCCCATGTTACC 2784 ACCAGGGCAACTGGGCAGGTTATTGCCAAACCAGAATTTACCACTTGACATCACATTGCA AAGCCCAACTGGTGCTGGACCTTTCCCAACCAATCAGAAACAGTAGTCCCTACTCAGTGAT 2878 ACCIATGAATICAAACTCCATGGGAAGACCAGGAGGAGTTATAATACTTCTTTACCCAG GCCACGCAGAGTTCGGCTGTGAGAGTCACCTGTGCTGCTACCACCAGTGCCATGAACCG 2938 ACCIGCACIGGGIGGCICTATICCCACATIGCCICTICGGICTAAIAGCATACCAGGI--3084 GCCAGTCCAAGGAGGTATGATTGGAACCCAGCAGCCAGCATCCCCATGAGGCCCAGCAG 3204 AGAGATGAACATGGGGGGACCTCAGTATAGCCAACAACAAGCTCCTCCAAATCAGACTGC ------CAGTATAACTTCTTGTGGGACGGAAATGTTGTCAAGCAGGAGCAGCTAAG GTGCACCAGCTCCACCATTCCTAGCTCAAGTCAAGAGAAGACCCTAAAATTAAGACAGA ACCTGTTGGAGCCCAGAAAACAGCACTGCGAATTTCACAGAGCACTTTTAATAACCCACG -------ATGCTCAAGTATGGGTGGGCCAAACCGAAATGTGACTGT GACTCAGACTCCTTCCTCAGGAGACTGGGGCTTACCAAACTCAAAGGCCGGCAGAATGGA 3144 CCAGCCTGGCCAAAGACAGACGCTTCAGTCTCAGGTCATGAATATAGGGCCATCTGAATT CCCCATGGGAATGGGGGCTAATCCCTATGGCCAAGCAGCAGCATCTAACCAACTGGGTTC 2190 2158 2250 2310 2329 2389 2484 2449 2544 2509 2664 2605 2724 2665 2725 2778 2818 2996 2545 2844 3112 9 9 ద g å g 8 ò g ð 8 g g 셤 유 ò å g ò g å g ç g ç õ 유 ద à ò õ à å

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This sequence represents a polynucleotide of the invention, and encodes a secreted protein. It was isolated from a human adult testis cDNA library, and is designated clone AJI. The DNA sequences and encoded polypeptides can be used as nutritional sources or supplements, or may shibit e.g. cytokine and cell proliferation/differentiation activity, immune stimilating or suppressing activity, haematopoiesis regulating activity, receptor/ligand activity, atti-inflammatory activity, activity, chemostatic/chemokinetic activity, cadherin/thmour invasion suppressor activity, tissue growth activity, tumour inhibition activity or other activities.

Sequence 462 BP; 140 A; 93 C; 106 G; 122 T;
                                                                              Secreted protein; nutritional source; cell proliferation activity; cell differentiation activity; immune stimulant; tissue growth activator; haematopoiesis regulator; anti-inflammatory; tumour invasion suppressor; tumour inhibitor; clone AJI_1; ds.
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                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotides - obtained from human adult testis, human adult ovary, human adult brain and human adult heart CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 462;
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Pred. No. 1.3e-107;
1; Mismatches 2;
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/note= "no stop codon given"
                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                       Agostino MJ, Jacobs K, Lavallie Racie LA, Spaulding V, Treacy M; WPI; 98-362424/31.
                                                   21-OCT-1998 (first entry)
Clone AJ1_1 5' coding sequence.
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                           standard; cDNA; 462
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Best Local Similarity 99.3
Matches 433; Conservative
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13-DEC-1996; US-766263.
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12-DEC-1997; U23224.
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Human, secreted protein; expressed sequence tag; EST; haematopolesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides encoding human secreted proteins - derived from
T. G. human blood, kidney, foetal lung, placenta, testes, brain,
T. e.g. human blood, kidney, foetal lung, placenta, testes, brain,
T. e.g. human blood, kidney, foetal lung, placenta, testes, brain,
T. claim 1; Page 487, 618pp; English.
T. claim 1; Page 487, 618pp; English.
The polynucleotide, which is a secreted EST, and the encoded protein
The polynucleotide, which is a secreted EST, and the encoded protein
The polynucleotide, which biological activities which would make
The predicted to have useful biological activities which would make
The me suitable for treating, preventing or ameliorating medical
Conditions in humans and animals, although no supporting data is
Given. Suggested activities include nutritional activity, immune
Atimulating or suppressing activity, haematopoiesis regulating
activity, tissue growth activity, activity, infinition
Coemic invasion suppressor activity, cancerivity, cadherin'thoughtion
Cotivity. The polynucleotide may also be useful for gene therapy.
Sequence 418 BP; 108 A; 114 C; 106 G; 90 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1208 GGATATAGACCAAAACCCAAATCCTGTTGGACAAGGGATTAGACCACCTATGGCTGGATGC 1267
141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 CAGAACAACAACTATGGGCTCAACATGAGTAGCCCCCCACATGGGAGTCCTGGTCTTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.7%; Score 392.4; DB 1
99.7%; Pred. No. 8.7e-97;
iive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                     V90274 standard; cDNA; 418 BP
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10-APR-1998; U06955.
10-APR-1997; US-838821.
(GEMY ) GENETICS INST INC.
                                                                                      2780 GGCTCAAGTATGGGTG 2795
                                                                                                                                                                                                                                                                                                                                                               15-FEB-1999 (first entry) EST clone D1454.
                                                                                                                         421 GGCTCAAGTATGGGAG 436
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Matches 393; Conservative
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RESULT

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therapeutic agents

Claim 18; Page 24; 38pp; English.

Char gequence encodes an epitope-tagged TATA-box binding protein (TBP)

Char is expressed by the transgenic non-human animals of the invention.

Characterise higher-order transcription complexes (from different tissue and cell types, optionally at different developmental stages). It is also used to identify new and/or specific TBP associated factors (TAFS, e.g. transcription factors, activators or inhibitors) and TAF-interaction factors, and to raise antibodies against TBP. The TAFS may be useful for regulating gene expression, e.g. disages-related genes, so are potential pharmaceuticals, also for identifying human analogues for use in drug screening. The antibodies are used for affinity purification of TBP and its complexes. TBP can isolate transcription complexes from a wide converted of different tissues and cells (contrast known methods that are limited to isolation from a particular cell type).

Sequence 1310 BP; 349 A; 357 C; 306 G; 298 T;
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Transgene for epitope tagged TBP protein.
TATA-box binding protein; epitope-tagged TBP; transcription complex; TAF;
TBP associated factor; TAF-interaction factor; gene expression regulator;
                                                                     Transgene for epitope tagged TBP protein.
TATA-box binding protein; epitope-tagged TBP; transcription complex; TAF;
TBP associated factor; TAF-interaction factor; gene expression regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3766 AGAGCTGCTAAGTCATCACTTCCGACAACAGGGGTGGCTATGATGATGCAGCAGCAGCAGCA 3825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transgenic animal expressing epitope-tagged TATA-box binding protein - for isolating higher-order transcription complexes and specific factors that associate with the protein, useful as potential
                                                                                                                                                                                                                                                                                                                                                       Berglund E, Kirschbaum B, Meisterernst M, Polites G;
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26-MAY-1998: 109516.
26-MAY-1997; EP-108433.
(FARH ) HOECHST AG.
Berglund E, Kirschbaum B, Meisterernst M, Polites (WPI; 99-001394/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.7%; Score 76.2; DB 1;
Best Local Similarity 74.4%; Pred. No. 8.4e-11;
Matches 96; Conservative 0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
  V08558 standard; cDNA; 1310 BP
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V08559;
                                             12-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                             26-MAY-1998; 109516.
26-MAY-1997; EP-108433.
(FARH ) HOECHST AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3886 AACCCAGGC 3894
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                                                                                                                                                                                                                                                                                                                                                                                  WPI; 99-001394/01
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EP-881288-A1.
02-DEC-1998.
                                                                                                                                                                                                       Synthetic.
EP-881288-A1.
02-DEC-1998.
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                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agostino MJ, Jacobs K, Lavallie ER, MCCoy JM, Merberg D,
Racie LA, Spaulding V, Treacy M;
Red JO70076/06.

New polynucleotides encoding human secreted proteins - derived from
e.g. human blood, Kidney, foetal lung, placenta, testes, brain,
F. cvary, pituitary, retina and colon cDNA libraries
F. Craim 1: Page 176: 633pp: English.

This sequence represents an expressed sequence tag (EST), and is a
colynucleotide of the invention. The polynucleotides of the invention are
colynucleotide of the invention. The polynucleotides of the invention are
colynucleotide of the invention. The polynucleotides of the invention
colon large sequences and proteins encoded by them are predicted to
colon section blological activities which would make them suitable for
colon activities allowed activity, immune stimulating or suppressing activity,
colon nutritional activity, immune stimulating or suppressing activity,
cactivity, cadherin/tumour invasion suppressor activity, tumour inhibition
colon thromobolytic activity, receptoryligand activity, the EST sequences are also stated to be useful for gene
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                                                                                                                                                                                                                                                                          EST clone AJI.

Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; human; chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis; receptor; ligand; anti-inflammatory; tumour inhibitor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2531 TCCATATCCTCAAATGGTAGTCATCTGGGGACTAAGCAACAGGTGTTTCAAGGAACTAAT 2590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2591 TCTCTGGGTTTGAAAGTTCACAGTCTGTGCAGTCTATTCGTCCTCCATATAACCGAGCA 2650
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Pred. No. 1.9e-61;
0; Mismatches 2; Indels 0
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                  79
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                                                                                                                                                                                                  V86262 standard; cDNA; 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1998.
10-APR-1998; U06954.
10-APR-1997; US-835913.
(GEMY.) GENETICS INST INC.
                                                                                                                                                                                                                                               27-APR-1999 (first entry)
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Best Local Similarity 99.2'
Matches 263; Conservative
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ID QE
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                                                                                                       claim 22; Page 25-27; 38pp; English.

This sequence encodes an epitope-tagged TATA-box binding protein (TBP)

This sequence encodes an epitope-tagged TATA-box binding protein (TBP)

that is expressed by the transgenic non-human animals of the invention.

Characterise higher-order transcription complexes (from different tissue and cell types, optionally at different developmental stages). It is also used to identify new and/or specific TBP associated factors (TAFs, e.g. transcription factors, activators or inhibitors) and TAF-interaction factors, and to raise antibodies against TBP. The TAFs may be useful for factors, also for identifying human analogues for use in drug screening. The antibodies are used for affinity purification of TBP and isolate transcription complexes from a wide its complexes. TBP can isolate transcription complexes from a wide immited to isolation from a particular cell type).

Sequence 4286 BP; 1017 A; 1133 C; 1160 G; 976 T;
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Claim 22: Page 27-29; 38pp; English.
This sequence encodes an epitope-taged TATA-box binding protein (TBP)
This sequence encodes an epitope-taged TATA-box binding protein (TBP)
That is expressed by the transgenic non-human animals of the invention.
The animals are used to produce TBP. TBP is used to isolate and
characterise higher-order transcription complexes (from different tissue
and cell types, optionally at different developmental stages). It is also
used to identify new and/or specific TBP associated factors (TAFs,
e.g. transcription factors, activators or inhibitors) and TAF-interaction
factors, and to raise antibodies against TBP. The TAFs may be useful for
regulating gene expression, e.g. disease-related genes, so are potential
pharmaceuticals, also for identifying human analogues for use in drug
screening. The antibodies are used for affinity purification of TBP and
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TATA-box binding protein; epitope-tagged TBP; transcription complex; TAF;
TBP associated factor; TAF-interaction factor; gene expression regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3766 AGAGCTGCTAAGTCATCACTTCCGACAAGAGGGTGGCTATGATGATGCAGCAGCAGCA 3825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transgenic animal expressing epitope-tagged TATA-box binding protein
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Lottors that associate with the protein, useful as potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.7%; Score 76.2; DB 1; Length 4286; 74.4%; Pred. No. 1.6e-10; tive 0; Mismatches 33; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.7
Best Local Similarity 74.4
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-1998; 109516.
26-MAY-1997; EP-108433.
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EP-881288-A1.
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PD 12-JAN-1995.
PD 29-JUN-1993; US-084365.
PR 29-JUN-1994; UO7336.
PR 29-JUN-1994; US-267803.
PR 28-JUN-1994; US-267803.
PR 28-JUN-1994; US-267803.
PP (MINU) 1994; US-267804.
PP (MINU) 1994; US-
its complexes. TBP can isolate transcription complexes from a wide variety of different tissues and cells (contrast known methods that are limited to isolation from a particular cell type).

Sequence 3263 BP; 860 AP; 794 C; 756 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3766 AGAGCTGCTAAGTCATCACTTCCGACAACAGGGGTGGCTATGATGATGCAGCAGCAGCA 3825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3768 AGCTGCTAAGTCATCACTTCCGACAACAGGGGTGGCTATGATGATGCAGCAGCAGCAAC 3827
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                                                                                                                                                                                                                                                                   Length 3263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.6%; Score 73.2; DB 1; Length 195; 99.7%; Pred. No. 2e-10; ve 0; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                33; Indels
                                                                                                                                                                                                                                                                   Score 76.2; DB 1;
Pred. No. 1.4e-10;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3888 CCCAGGCCTTCAGCCCACCTCC 3909
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                                                                                                                                                                                                                                                                        1.78;
74.48;
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Best Local Similarity 69.77
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                96; Conservative
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Best Local Similarity
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WO9501437-A.
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3768 AGCTGCTAAGTCATCACTTCCGACAACAGAGGGTGGCTATGATGATGCAGCAGCAGCAAC 3827
                                                                                                                                                                                  Chung M. Orr H. Zoghbi HY;
WPI; 95-061001/08.

New autosomal dominant spinocerebellar ataxia type I nucleic acid diagnosis of a SCA1 disorder.

Lused to develop prods. for detection or presymptomatic diagnosis of a SCA1 disorder.

Disclosure; Fig 2; 111pp; English.

094831-084835 show the CAG repeat regions of five individuals affected with spinocerebellar ataxia type I (SCA 1). It is within CAG repeat region (Q84804) that the mutations responsible for SCA I occur. The full nucleic acid (Q84793) and its protein product (R71111) can be used to develop products, for the presymptomatic detection of a SCA I disporder.

Sequence 171 BP; 52 A; 59 C; 56 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-SEP-1995 (first entry)
Spinocerebellar ataxia type 1 CAG repeat region patient #4.
Spinocerebellar ataxia type 1; SCA 1; presymptomatic diagnosis; CAG repeat region; patient #4; ss.
            Length 168;
                                                                 Indels
      Score 73.2; DB 1;
Pred. No. 1.8e-10;
0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                    3888 CCCAGGCCTTCAGCCCACCTCC 3909
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                                                                                                                                                                                                                                                                                                                                                                                                                                137 AGCAGCACCTCAGCAGGCTCC 158
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   1.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q84834 standard; DNA; 171 BP
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Best Local Similarity 69.77
Matches 99; Conservative
                                                                 Conservative
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29-JUN-1994; U07336.
29-JUN-1993; US-084365.
28-JUN-1994; US-267803.
(MINU ) UNIV MINNESOTA.
                                  Similarity
Ouery Match
Best Local Simi
Matches 99;
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29-JUN-1994; UG-084365.
29-JUN-1994; UG-084365.
29-JUN-1999; UG-084365.
29-JUN-1999; UG-084365.
29-JUN-1999; UG-084365.
28-JUN-1999; UG-084365.
28-JUN-1999; UG-084365.
28-JUN-1999; UG-084365.
29-JUN-1999; UG-084365.
20-JUN-1999; UG-084365.
20-JUN-1999; UG-084369.
20-JUN-1999; UG-08439.
20-J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure: Fig 2: 111pp: English.
084811-084815 show the CAG repeat regions of five individuals
affected with spinocerebellar ataxia type 1 (SCA 1). It is within
CAG repeat region (084804) that the mutations responsible for
SCA 1 occur. The full nucleic acid (084793) and its protein product
(R71111) can be used to develop products, for the presymptomatic
detection of a SCA 1 disorder. 73 A 80 C; 77 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                          used to develop prods. for detection or presymptomatic
                     Spinocerebellar ataxia type 1 CAG repeat region patient #2. Spinocerebellar ataxia type 1; SCA 1; presymptomatic diagnosis; CAG repeat region; patient #2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spinocerebellar ataxia type 1 CAG repeat region patient #3.
Spinocerebellar ataxia type 1; SCA 1; presymptomatic diagnosis;
CAG repeat region; patient #3; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.6%; Score 73.2; DB 1; Length 234; llarity 69.7%; Pred. No. 2.2e-10; Conservative 0; Mismatches 43; Indels (
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29-JUN-1993; US-084365.
28-JUN-1994; US-267803.
CHUND ) UNIV MINNESCORA.
CHUND ) OTF HT, Zoghbi HY;
WPI; 95-061001/08.
New autosomal dominant spinocerebellar ataxia type 1 r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q84833 standard; DNA; 168 BP
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(first entry)
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Best Local Similarity
Matches 99; Conserv
                                                                                                                   Homo sapiens.
W09501437-A.
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WO9501437-A.
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Q84833; 25-SEP-1995

ö T42476/c ID T42476 standard; DNA; 645 BP. AC T4476; DT 01-AUG-1997 (first entry) DE HuntL4 coding sequence. KW HuntL4 coding sequence. KW HuntL1, HuntL4; huntington's disease; IT15; Huntington gene; gene therapy; KW HuntL1, HuntL4; huntington's disease; HD; autosomal dominant; neurodegenerative disease; 3768 AGCTGCTAAGTCATCACTTCCGACAACAGGGTGGCTATGATGATGCAGCAGCAGCAAC 3827 0; Gaps 1.6%; Score 73.2; DB 1; Length 171; 69.7%; Pred. No. 1.8e-10; tive 0; Mismatches 43; Indels

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KW non-insulin dependent diabetes mellitus; hypertension; norepinephrine; KW inhibitor; alpha-adrenergic receptor; epinephrine; ss.

Normo sapiens:

Location/Qualifiers

FT cds //transl_except (pos: 235. 237, aa: Cys)
FT //transl_except (pos: 241. 244, aa: Arg)
FT //transl_except (pos: 250. 252, aa: Leu)
FT //transl_except (pos: 282. 384, aa: Arg)
FT //transl_except (pos: 282. 384, aa: Arg)
FT //transl_except (pos: 382. 384, aa: Arg)
FT //transl_except (pos: 382. 384, aa: Arg)
FT //transl_except (pos: 262. 384, aa: Arg)
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FT //transl_except (pos: 382. 382. 382. 384, aa: Arg)
FT //transl_except (pos: 382. 382. 382. 384, aa: Arg)
FT //transl_except (pos: 382. 38
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Query Match 1.5%; Score 68.6; DB 1; Length 645; Best Local Similarity 74.8%; Pred. No. 6.6e-09; Matches 86; Conservative 0; Mismatches 29; Indels (

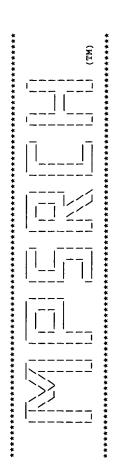
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Search completed: September 18, 1999, 01:53:32 Job time: 18531 sec

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protein - protein database search, using Smith-Waterman algorithm Fri Sep 17 21:02:33 1999; MasPar time 48.85 Seconds 616.024 Million cell updates/sec MPsrch_pp

Tabular output not generated.

>US-09-041-994-2 (1-1415) from US09041994.pep 9849 Description: Perfect Score: Sequence:

1 MSGLGENLDPLASDSRKRKL.....MNMNPMPMSGMPMGPDQKYC 1415

170751 segs, 21266608 residues Searched:

PAM 150 Gap 11

Scoring table:

Minimum Match 0% Listing first 45 summaries Post-processing:

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part33 33:part34 35:part35 36:part36 37:part37 38:part38

Mean 39.485; Variance 214.637; scale 0.184 tatistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

					CHITAGA		
		æ					
Result		Query					
Ñ.	Score	Match	Match Length DB	DB	ΙD	Description	Pred. No.
-	3346	34.0	1464	30	W42632	Human transcriptional	2.04e-248
7	914	9.3	147	34	W69239	Clone AJ1 1 protein s	1.24e-57
~	643	6.5	1061	24	W26370	Human steroid recepto	6.23e-37
4	232	2.4	846	37	W79533	Human CLOCK protein.	7.96e-07
S	232	2.4		14	R80551		7.96e-07
Q	232	2.4	848	23	W25668	Human Ah-receptor.	7.96e-07
7	235	2.4	855	37	W79529	Mouse CLOCK protein.	4.96e-07
ω	225	2.3	371	38	W73369	Epitope tagged TBP pr	2.39e-06
σ	231	2.3	805	14	R80561	Murine Ah receptor pr	9.32e-07
10	213	2.2	1313	33	W60213	Spinocerebellar ataxi	1.56e-05
11	202	2.1	539	30	W33628	Yeast transcriptional	8.55e-05
12	209	2.1	594	34	W68092	Mouse neuronal PAS do	2.90e-05
13	210	2.1	800	14	R84883	Transcription factor	2.48e-05
14	202	2.1	870	27	W37097	Human endothelial PAS	8.55e-05
15	203	2.1	914	25	W24800	Spinocerebellar ataxi	7.33e-05
16	203	2.1	1312	30	W33807	Human ataxin-2.	7.33e-05

	38e-0	.38e-0	.28e-0	. 28	•	. 28	3.39e-04	33	.91e	.36	'n	. 50	6)	8	1.84e-04	1.16e-04	•	6.24e-04	1.33e - 03	.33	. 55	. 24	4	.36	36	6.24e-04	6.24e-04
Cellular transcriptio Transcription factor	. ~	CREB binding protein.	Protein encoded by Hu	Human huntingtin prot	Human huntingtin.	Previously undescribe	Polyoma virus enhance	virus	Alternatively spliced	onal PA	Osf2/Cbfal native pol	(single	prot	Deltex protein.	Drosophila Deltex pro	ne endothelial	protei	HIF-1 alpha delta-NB	Drosphila melanogaste	Human h-NUMB-R.	D. melanogaster dorsa	ŭ	Hypoxia inducible fac	Mouse neuronal PAS do	Spinocerebellar ataxi	Amino acid sequence o	Human hypoxia inducib
W40057 R84882	W40058	R79054	R58777	W44742	W09871	W36887	R75454	R75453	W89189	W68091	W89184	W30758	R76639	R76640	W18317	W37098	W41372	W06559	W48796	W83215	R42087	W39927	W06558	W68094	R71111	4	W06557
30	30	14	ī	53	22	56	14	14	39	34	33	25	13	15	23	27	30	20	32	37	œ	29	20	~	_	36	\sim
2414	2441	2441	3144	3144	3144	3144	306	513	548	290	596	657	737	737	737	875	81	373	591	609	678	789	802	816	816	826	826
2.1	2.1	2.1	2.1					•	•	•						2.0	1.9	1.9		1.9	1.9	1.9	1.9	1.9	1.9	1.9	1.9
210	205	202	204	204	204	204	193	193	.194	199	194	195	197	197	197	200	190	189	184	184	183	189	189	190	190	189	189
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                                                                                                                                                                            New isolated transcriptional intermediary factor-2 - useful in assays for drugs which are capable of enhancing or inhibiting unclear receptor—rediated pathways

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44.1%; Pred. No. 2.04e-248;
ative 370; Mismatches 318;
                                                                                                                 Chambon P, Gronemeyer H, Lutz Y, Voegel
WPI; 98-110525/10.
N-PSDB; V03517.
12-JUL-1996; US-021247.
(BRIM) BRISTOL-MYERS SQUIBB CO.
(CORE) CENT NAT RECH SCI.
(INRM) INST NAT SANTE & RECH MEDICALE.
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Matches 653; Conservative
                                                                                              PASTEUR LOUIS
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11-OCT-1998 (first entry)
Licone All_1 protein sequence.
Secreted protein; nutritional source; cell proliferation activity;
cell differentiation activity; immune stimulant; tissue growth activator;
hemantopolesis regulator; anti-inflammatory; tumour invasion suppressor;
tumour inhibitor; clone AJ1_1.
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                                                                                                                                                                                                                                                                 This sequence is secreted protein, encoded by a polynucleotide of the invention. The DNA was isolated from a human adult testis cDNA library, and is designated clone AJI_1. The DNA sequences and encoded polypeptides can be used as nutritional sources or supplements, or may exhibit e.g. cytokine and cell proliferation/differentiation activity, inceptor/ligand activity, anti-inflammatory activity, activity, anti-inflammatory activity, activity, chemostatic/chemokinetic activity, chamour invasion suppressor activity, tissue growth activity, tumour inhibition activity or other activity, tissue growth activity, sequence 147 AA,
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                                                                                                                                                                                         New isolated polynucleotides - obtained from human adult testis, human adult ovary, human adult brain and human adult heart cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 914; DB 34; Length 14
Pred. No. 1.24e-57;
0; Mismatches 0; Indels
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Steroid receptor coactivator-1; SRC-1; molecular switch;
gene therapy; transgenic animal.
                                                                                                              Agostino MJ, Jacobs K, Lavallie ER, Mccoy JM, Merberg Racie LA, Spaulding V, Treacy M; 98-362424/31.
                                                                                                                                                                                                                                                   Claim 8; Page 62-63; 108pp; English.
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W26370 standard; Protein; 1061 AA.
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Best Local Similarity 100.0%;
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                                12-DEC-1997; U23224.
11-DEC-1997; US-989232.
13-DEC-1996; US-766263.
(GEMY ) GENETICS INST INC.
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WO9710337-A1.
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456 mdgavtsvtikseilpaslqsatarptsrln-rlpeleleaidnqfgqpgtgdqi-pwtn 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; Fig 14.1-14.3; 154pp; English.
This is the amino acid sequence of human CLOCK protein, an integral component of the circadian clock that serves to regulate various
an SRC-1 coding region for use in gene therapy. Transcription of target gene can be decreased by providing a nucleic acid encoding dominant-negative inhibitor of a SRC-1 polypeptide in a cell containing the target gene (also claimed).

Sequence 1061 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 572 dralgidklv-qgggldvlserfppqqatpplimeerpnlysqpysspfptanlpspfqg
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                                                                                                                                                                                                                                                                                                                                                                                                                            631 mvrqkpslgtmpvqvtpprgafspgmgmgprqtlnrppa-apnglrlglgqrlgggggli
                                                                                                                                                                                                                                                                                                              514 ntvtaingsk-sedgci-ssgldellcppttvegrndekalleglvsflsgkdetelael
                                                                                                                                  Score 643; DB 24; Length 1061;
Pred. No. 6.23e-37;
89; Mismatches 89; Indels 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLOCK; circadian rhythm; human; jet-lag; sleep-wake disorder; seasonal affective disorder; cancer; transcription factor;
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/label= bHLH
/note= "basic helix-loop helix domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Claimed fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .r 4
W79533 standard; Protein; 846 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-1997; US-885291.
13-MAR-1997; US-816693.
10 UNIV NORTHWESTERN.
Pinto LH, Takahaski JS, Turek F; WPI; 98-520828/44.
N-PSDB; V61450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAS-A
                                                                                                                                ch 6.5%;
1 Similarity 36.2%;
113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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/label- P
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13-MAR-1998; U05114
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02-FEB-1999
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4

848 AA;

Sequence

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Pollutants
Claim 3; Column 41-48; J4pp; English.

Claim 41-48; Claim 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human Ah receptor protein.
Mouse Ah receptor; drug; carcinogen; toxic agent; probe; human; bioassay;
C57BL/6J mouse liver; environmental pollutant; recombinant organism;
aspects of circadian rhymth, including intrinsic circadian period and the persistence of circadian rhythmicity. The sequence was deduced from the isolated clock gene (see Vol450). Mouse CLOCK (see W79529) is also claimed. CLOCK is a member of the bHLH-PAS domain family of proteins, and thus likely interacts directly with DNA.

It has Gln., Pro. and Ser-rich C-terminal regions characteristic of activation domain transcription factors. The invention provides isolated and purified CLOCK polypeptides, polynucleotides, vectors in host cells. The polynucleotides, polynucleotides, vectors is and host cells. The polynucleotides or polypeptides can be used to treat disorders of altered or disrupted circadian rhythms e.g. treat disorders altered or disrupted circadian rhythms e.g. such as mood state, stress, neurological disorders, to regulate diet and food intake aspecially for diababets, to treat candowascular, respiratory, liver or endocrine disorders, and for diagnosis and treatment of abnormal cell division such as cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  generate recombinant organisms useful as blomonitors for environmental pollutants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -rgd--wk-ptflsneeftqlmlealdgfflaimtdgsijyvsesvtsllehlpsdlvdg 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 RREQESKYIEELAELISANLSDIDNFNV-KPDKCAILKETVRQIRQIRGGKTISNDDDV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 rnksekkrrdqfnvlik-elgsmlpgnarkmdkstvlqksidflrkhkel-taqsdasel 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used in competitive binding assays to detect environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 232; DB 37; Length 84:
Pred. No. 7.96e-07;
48; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 sifnfipegehsevykilsthllesdsltpeylksknglefcchml 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |::|:: | :: : | |: :: | |: |:|| SVYNILHEEDRRDFLKNLPKSTVNGVSWTNEPQRQKSH-TFNCRML 200
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08-APR-1993; US-045806.
(NOUN) UNIY NORTHWESTERN & FOUND.
(WISC ) WISCONSIN ALUMNI RES FOUND.
Bradfleld (A, Dolwick KM, Poland A; WPI; 95-051315/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R80551 standard; Protein; 848 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 27.7%;
Matches 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  846 AA;
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R8
DT 29
DDT 29
KW MO
KW C5
KW C5
PN US
PN US
PF 08
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New genetically engineered yeast and mammalian cells - contain the Ah receptor gene and a reporter gene, used for detecting Ah receptor gene and a reporter gene, used for detecting Ah receptor geneits, particularly environmental pollutants

Claim 1: Fig 6: 47pp; English.

This sequence represents the human Ah receptor molecule. The cDNA encoding this protein may be used to transform a viable yeast cell, which may also be transformed with a plasmid expressing an Ah receptor nuclear translocator, a dioxin responsive element and a reporter gene. The reporter gene detects the activation of the Ah receptor upon the binding of agonists to the Ah receptor. The transformed cells can be used to detect and soil or in tissue samples. They can be used for detecting and monitoring environmental pollutants such as dioxin.
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                                                                                                                                                                                                                                                                                                    83 fdvalksspterngggdncraanfreglnlge-gefllgalngfvlvvttdalvfyasst 141
                                                                                                                                                                                                                                                                   83 fdvalksspterngggdncraanfreglnlge-gefllgalngfvlvvttdalvfyasst 141
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                                                                                                                                   27 paegiksnpskrhrdrlnteldrlasllp--fpq-dvin-kldklsvlrlsvsylraksf 82
                                                                                                                                                                                               25 PGGGLTCSGEKRRREQESKYIEELAELISANLSDIDNFNVKPDKCAILKETVRQIR- 83
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Ah receptor; yeast; nuclear translocator; reporter gene;
                                                                   <u>ئ</u>
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   Length 848;
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Pred. No. 7.96e-07;
52; Mismatches 50; Indels
Score 232; DB 14; Length 84 Pred. No. 7.96e-07; 52; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dioxin responsive element; environmental pollutant.
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113..400
/note= "PAAS domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                    142 iqdylgfqqsdvihqsvyelihtedraefqrql 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dolwick KM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Basic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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W25668 standard; Protein; 848
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2.4%;
Best Local Similarity 27.5%;
Matches 42; Conservative
Query Match
Best Local Similarity 27.5%;
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W25668;
05-NOV-1997 (first entry)
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(NOUN ) UNIV NORTHWESTERN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 045806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Ah-receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bradfield CA, Car.
WPI; 97-384667/35.
N-PSDB; T85436.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-APR-1993;
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This is the amino acidy degrees of mouse CLOCK protein, an integral component of the circadian clock that serves to regulate various aspects of circadian rhymth, including intrinsic circadian period and the persistence of circadian rhythmicity. The sequence was accounted from the isolated Clock gene (see V61401). Human CLOCK (see W79533) is also claimed. CLOCK is a member of the billin-PsA domain family of proteins, and thus likely interacts directly with DNA. It has Gln., Pro- and Ser-rich C-terminal regions characteristic of activation domain transcription factors. The invention provides isolated and purified CLOCK polypeptides, polynucleotides, vectors and host cells. The polynucleotides or polypeptides can be used to treat disorders of altered or disrupted circadian rhythms e.g. isolated and purified GLOCK polypeptides. Polynucleotides can be used to treat disorders of altered or disrupted circadian rhythms e.g. jet-lag, seasonal affective disorder, sleep-wake cycle disorders cuch as mood state, stress, neurological disorders, to regulate circadian challents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rnksekkrrdgfnvlik-elgsmlpgnarkmdkstvlgksidflrkhke-ttagsdasei 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel mouse and human circadian rhythm gene, clock - useful for treating e.g. jet-lag, sleep-wake disorders, abnormal cell division,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Gaps
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                                                                                                                     CLOCK; circadian rhythm; mouse; jet-lag; sleep-wake disorder; seasonal affective disorder; cancer; transcription factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 235; DB 37; Length 855; Pred. No. 4.96e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35..81
/label- bHLH
/note= "basic helix-loop helix domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "deleted in mutant CLOCK"
                                                                                                                                                                                                                                                                                          2..855
/note= "Claimed fragment"
                                                                                                                                                                                                                                                                                                                                             10..855
/note= "Claimed fragment"
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11..855
/^rte= "Claimed fragment"
                                                                                                                                                                                                                                                            Location/Qualifiers
W79529 standard; Protein; 855 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUN-1997; US-885291.
13-MAR-1997; US-816693.
(NOUN) UNIV NORTHWESTERN.
Pinto LH, Takahaski JS, Turek F;
WPI; 98-520828/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 18; Fig 12; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= PAS-A
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514..564
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Best Local Similarity 27.7%;
Matches 46; Conservative
                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..163
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                                                                                              Mouse CLOCK protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-MAR-1998; U05114.
                                                                                                                                                                                            diagnosis; therapy
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                              W79529;
02-FEB-1999
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A PAC 
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Therapeutic agency
Claim 5: Page 20-22: 38pp; English.
Claim 6: Pa
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2-NOV-1995 (first entry)
Murine Ah receptor protein.
Mouse Ah receptor; drug: carcinogen; toxic agent; probe; human; bloassay;
C57BL/6J mouse liver; environmental pollutant; recombinant organism;
                                                                                                                                                                                                         TATA-box binding protein; epitope-tagged TBP; transcription complex; TAF;
TBP associated factor; TAF-interaction factor; gene expression regulator.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic animal expressing epitope-tagged TATA-box binding protein - for isolating higher-order transcription complexes and specific factors that associate with the protein, useful as potential
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Pred. No. 2.39e-06;
16; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 SVYNILHEEDRKDFLKNLPKSTVNGVSWTNEPQRQKSH-TFNCRML 200
                                                                                                                                                                                                                                                                                                                                                                                                                                    Berglund E, Kirschbaum B, Meisterernst M, Polites G; WPI; 99-001394/01.
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/product= mouse Ah receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-APR-1993; US-045806.
(NOUN ) UNIV NORTHWESTERN & FOUND.
(WISC ) WISCONSIN ALUMNI RES FOUND.
Bradfield CA, Dolwick KM, Poland A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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R80561 standard; Protein; 805 AA.
                                                                        л 8
W73369 standard; peptide; 371 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.3%;
Local Similarity 38.5%;
Los 42; Conservative
                                                                                                                              W73369; 12-FEB-1999 (first entry)
Epitope tagged TBP protein.
                                                                                                                                                                                                                                                                                                                                                02-DEC-1998.
26-MAY-1998; 109516.
26-MAY-1997; EP-108433.
(FARH ) HOECHST AG.
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08-APR-1993; 045806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          therapeutic agents
                                                                                                                                                                                                                                                                                                          EP-881288-A1.
                                                                                                                                                                                                                                                               Homo sapiens
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Green MR, Reese JC;
WPI; 98-077189/07.
N-PSDB; V04771.
               Query Match
Best Local Similarity
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                                                                      Claim 1; Column 31-36; 24pp; English.

The amino acid sequence of the murine Ah receptor protein. The Ah receptor is a soluble protein which mediates an individuals response to a variety of drugs, carcinogens and toxic agents. The gene was isolated from a mouse genomic DNA library using the probes 099603-5. These probes were determined from the N-terminal sequence of a purified Ah receptor, which was purified from C57BL/6J mouse liver. The screen isolated a clone designated cAhl containing the full length cDNA. The 1.4 kb fragment of the murine clone was used to obtain clones covering the coding sequence of the human AH receptor (099602). The Ah receptors are useful in bioassays to detect environmental pollutants. The genes can be environmental pollutants.

Sequence 805 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This is the protein sequence of a gene causative of spinocerebellar atlast is the protein sequence of a gene causative of spinocerebellar atlastia type 2 (SCA2), a neurodegenerative disease. The gene associated with SCA2, has a tri-nucleotide (CAG) repeat region which in the expression product produces a polyglutamine sequence from Gln-166 to Gln-188. In the normal gene there are 15-25 CAG repeats but in SCA2 patients this number is increased to 35-100. Peptides encoded by nucleic acid fragments (DNA or RNA) containing sequences from the SCA2 associated hybridising with the nucleic acid fragments can be used for the investigation and diagnosis of SCA2. They can also be used for the treatment of SCA2 by antisense therapy or gene therapy.
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02-0CT-1998 (first entry)
Spinocerebellar ataxia type 2 (SCA2) disease associated protein.
Spinocerebellar ataxia type 2; SCA2; gene therapy; antisense therapy;
CAG repeat; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                   82 fdvalkstpadrnggqdqcraq-irdwqdlqegefllqalngfvlvvtadalvfyassti 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SS QGKII-SNDDDVQKADVSSTGQGVIDKDSL--GPLLLQALDGFLFVVNREANIVFVSENV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid fragments associated with spinocerebellar ataxia type 2 - contain increased number of CAG repeat region compared to normal
                                                                                                                                                                                                                                                                                                                                                                                                    25 PGOGLICSGEKRRREQESKYIEELAELISANLSDIDNFNVKPDKCAILKETVRQIRQIKE 84
                                                                                                                                                                                                                                                                                                                                                                       26 paegiksnpskrhrdrinteldriaslip--fpq-dvin-kidkisvirisvtylraksf 81
                                                                                                                                                                                                                                                                                                                                              Gaps
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/note= "Glutamine rich region; this region is
increased in SCA2 patients"
                               encoding murine and human Ah receptors
                                                                                                                                                                                                                                                                                                         Score 231; DB 14; Length 805;
Pred. No. 9.32e-07;
46; Mismatches 52; Indels
                           Nucleic acid sequences encoding murine and human Ah receptused in competitive binding assays to detect environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               141 qdylgfqqsdvihqsvyelihtedraefqrql 172
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                                                                                                                                                                                                                                                                                                           Ouery Match 2.3%;
Best Local Similarity 30.3%;
Matches 46; Conservative
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30-0CT-1997; J03946.
30-0CT-1996; JP-304059.
(SRLS.) SRL INC.
Sanpel K, Tsuji S;
WPI: 98-272215/24.
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                                                           pollutants
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This polypeptide comprises a 68 kDa yeast transactivating factor,
TAF-68, that is associated with the TAFA-box binding protein.

TAF-68 that is associated from Saccharomyces creevisiae cells by
virtue of its affinity to fungal or human TATA-box binding proteins
using chromatographic procedures. It can also be recombinantly
produced in host cells utilising vectors carrying a TAF-47 nucleic
acid (see V04771). The yeast TAF complex includes 9 polypeptides
cof 180, 145 (see W33622), 116, 90 (see W33634), 68, 62, 51-54, 47
(see W33627) and 30 kDa. At least some of these are required for
transcription in vitro. TAFs are also essential for viability.

TAF-68 can be used in the discovery, design and development of
antifungal agents, e.g. for treatment of candida albicans infections
(candidaesis). It can also be used to raise diagnostically useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::1 :::1 | : ::| | : ::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : ::::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : ::::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : :::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| | : ::| |
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                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W33628;
06-JUL-1998 (first entry)
Yeast transcriptional activator factor, transactivating factor;
TAF-68; transcriptional activator factor; transactivating factor;
TATA-box binding protein-associated factor; yeast;
transcription; viability; antifungal; fungicide; infection;
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Mouse neuronal PAS domain protein NPASI.
NPASI; neuronal bHLH-PAS domain; mouse; transcription factor;
           Length 1313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 202; DB 30; Length 539;
Pred. No. 8.55e-05;
12; Mismatches 25; Indels
                                                                                                                Indels
Score 213; DB 33; I
Pred. No. 1.56e-05;
14; Mismatches 10;
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1..134
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W68092 standard; Protein; 594 AA.
W68092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W33628 standard; Protein; 539 AA.
2.2%;
llarity 55.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-DEC-1997.
26-JUN-1997; U11144.
26-JUN-1996; US-673234.
(UYMA-) UNIV MASSACHUSETTS.
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Best Local Similarity 47.3%;
Matches 35; Conservative
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W37097;
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                                                                                                                                                                                                                                                New isolated neuronal PAS domain proteins - can regulate function of neurological tissue such as brain tissue, used to develop products of condagnosis and therapy

Tor diagnosis and therapy

Claim 1: Page 29-31; 42pp; English.

This is the amino acid sequence of mouse neuronal PAS domain protein

RASI, a new member of the basic helix-loop-helix (PHILH)-PAS family

of transcription factors. A database search for expressed sequence

tags bearing sequence similarity to the PAS domain of the aryl

of transcription factors of Adatabase search for expressed sequence

tags bearing sequence similarity to the PAS domain of the aryl

of transcription factor of hybridisation probes, and clones

primers for PCR amplification of hybridisation probes, and clones

(see V41245-59) coding for human and mouse NPAS proteins (see

primers for PCR amplification of hybridisation probes, and clones

(see V41245-94) were selected from mouse brain tissue. They can be produced

tissue and Hela cells. The NPAS proteins can regulate the function

of neurological tissue such as brain tissue. They can be produced

crecombinantly from transformed host cells or purified from

mammalian cells. NPAS proteins and polypurclectides can be used in

diagnosis (e.g. genetic hybridisation screens for NPAS transcripts),

the biopharmaceutical industry (e.g. as immunogens, reagents for

sorreening chemical libraries for lead pharmacological agents).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 rrgpvalvse-vfeqh-lgghilqsldgfvfalnqegkflyisetvsiylglsqveltgs 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SERING SERING SERVICE SERVICE SERVICENCY SER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 SVYNILHEEDRKDFLKNLPKSTVNGVSWTNEPQRQKSHTFNCRMLMKTPHDILEDINASP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eckner R, Ewen M, Livingston D;
WPI: 95-373813.48.
Nucleic acid encoding human p300 that associates with adenovirus ElA
- and related vectors, host cells and screening assays, also
diagnosis of cancerous and pre:cancerous tissue by detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A fusion protein comprising glutathione-S-transferase and amino acids 1572-2371 (R84883) of human transcription factor p300 (full sequence given in R84882) was used to produce an anti-p300 monoclonal antibody (MAb) useful in identifying p300 binding proteins and for characterizing p300 in immunoassays. Sequence 800 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 3;
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Transcription factor p300 C-terminal (1572-2371) region.
Transcription factor; p300; adenovirus; early region 1A; ElA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 209; DB 34; Length 594;
Pred. No. 2.90e-05;
35; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; monoclonal antibody.
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Claim 17; Page 72-78; 126pp; English.
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14-APR-1994; US-227536.
(DAND ) DANA FARBER CANCER INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R84883 standard; Protein; 800 AA.
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Best Local Similarity 28.5%;
Matches 35; Conservative
                                21-JAN-1998; U01154.
21-JAN-1997; US-785310.
(TEXA ) UNIV TEXAS SYSTEM.
                                                                                                                                                McKnight SL, Russel DW;
WPI; 98-414103/35.
                                                                                                                                                                                                                                N-PSDB; V41257
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WO9528499-A1.
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regulators, e.g. a heat shock protein.

Tequilators, e.g. a heat shock protein.

Claim 1; Columns 25-30; 23pp; English.

The present sequence represents a novel human endothelial PAS domain protein an a represent sequence represents an expension of protein and be used in a screening assay for agents that concein can be used in a screening assay for agents that modulate binding of EPAS1 to a binding target, especially a basic helix-loop-helix (BHIH)/PAS protein, a heat shock protein or hypoxia inducible factor (HFF 1 alpha) binding site. The EPAS1 protein is inducible factor (HFF 1 alpha) binding site. The EPAS1 protein is concusted with the binding target and a test agent and the effect of the test agent on the binding affinity of the protein for the target is determined. The proteins may be produced recombinantly from transformed constitution screens for EPAS1 transcripts), therapy (e.g. gene therapy concurred to meanmalian cells. The proteins may be used in diagnosis (e.g. gene therapy concurred to meanmal the effect of the proteins are sensitive in the biopharmaceutical industry (e.g. as immunogens, reagents for industry for screening charactors or other transcriptional regulators, reagents for screening chemical libraries for lead pharmacological agents, etc.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human endothelial PAS domain protein 1 (EPAS1).

Endothelial PAS domain protein 1; EPAS1; screening assay; gene therapy;
Endothelial tissue specification; EPAS1 binding; heat shock protein;
basic helix-loop-helix motif; bHIH; hypoxia inducible factor;
HIF-1 alpha binding site; binding affinity; genetic hybridisation screen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1201 GGA--AVMR--PMMQPQQGFLNAQMVAQRSRELLSHHFRQ-QRVAMMMQQQQQQQQQQQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1256 QQQQQQQQQQQQQQQQQQDAFSPPNVTASPSMDGLLAGPTMPQAPPQQFPYQPNYGMGQQPDPA 1315
                                                                                                                                                                                                                                                                                                                                                                                                                             1025 QNRPLLRNSLDDLVGPPSNLEGQSD-ERALLDQLHTLLSNTDATGLEEIDRALGIPE-LV 1082
                                                                                                                                                                                                                                                   972 RPVLQQQQQMLQMRP-G-EIP-MGMGANPY---GQAAAS-NQLGSWPDGMLSMEQVSHGT 1024
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                                                                                                                                                                         379 rpiqhqmppmtpmapmmtrgpsghlepgmgptgmqqqppwsqgglpqqqlqsg 438
                                                                                                                                                                                                                                                                                                                                               494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endothelial PAS domain protein 1 proteins - used for isolating EPAS1 regulators, e.g. a heat shock protein
                                                                                                                                                                                                                                                                                                                                               439 mprpamm-svaqh-gqplnmapqpglgqvgisplkp--gtvsqqalqnllrtlrspsspl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                495 qqqqvl-silha-npqllaafikqraakyansnp-qpipgqpgmp-qqq-pglqpptmpg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qqgvhsnpamqnmnpmqagvq-raglp-q-q-qpqqqlq-ppmggmspqaqqmnmnhntm
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Score 210; DB 14; Length 800;
Pred. No. 2.48e-05;
91; Mismatches 167; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1316 F-GR-VSSP-PNAMMSSRMGPSQNPMMQHPQAAS 1346
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W37097 standard; Protein; 870 AA.
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17-JAN-1997; US-785241.
17-MUNIV TEXAS SYSTEM.
MCKNIGHT SL, RUSSELL DW, TIAN H;
WPI; 98-041300/04.
    Query Match 2.1%;
Best Local Similarity 25.6%;
Matches 101; Conservative
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Og-FEB-1998 (first entry)
Spinocerebellar ataxia SCA2 protein A.
Spinocerebellar ataxia SCA2 protein A.
Monoclonal antibody: neurodegenerative disease; polyglutamine; TBP;
repeat region; affinity; TATA binding protein; Kennedy disease;
transcription initiation factor; lymphoblastic cell line; schizophrenia;
Huntington's disease; dominant autosomal spinocerebellar ataxia;
X-linked spino-bulbular muscular atrophy; familial spastic paraplegia;
manic depressive psychosis.
                                                                                Gaps 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..80
/note= "this region may be encoded by an open reading
frame not conatained in SCA2 but in frame with
it"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treatment of neurodegenerative diseases associated with the presence of polyglutamine repeat regions. This MAD is already known for its affinity to the TATA binding protein (TBP) transcription initiation factor, especially at the amino acid sequence LEEQORQOQQQ found at the N-terminus of TBP. MAD IC2 has been shown to have a high affinity for polyglutamine repeats with a proportional affinity to the number of glutamine repeats. This affinity has been used to identify genes encoding proteins containing long polyglutamine repeats which are implicated in neurodegenerative diseases. A screen of an expression stibrary, generated from a lymphoblastic cell line from a patient
                                                                                                                   71 ssvcseneseaeadqqmdnlylkalegfiavvtqdgdmiflseniskfmgltqveltghs 130
                                                                                                                                              98 ADVSSTGGGVIDKDS-LGPLLLQALDGFLFVVNREANIVFVSENVTQYLQYKQEDLVNTS 156
                                                                                                                                                                                                131 ifdfthpcdheeirenlslkngsgfg-kkskdmsterdffmrmkctvtnrgrtvnlksat 189
                                                                                                                                                                                                                         190 wkvlhctgqvkvynncpphnslcgykepllscliimcepighpshmdipldsktflsrhs 249
                                                                                                                                                                                                                                                                                                       250 mdmkftycd-dri-teli-gyhpeellgrsayefyhaldsen-mtksh-qnlctkggvvs 304
                                                                                                                                                                                                                                                                                                                                                                                                273 LSGKVVNIDTNSLRSSMRPGF--EDIIRRCIQRFFSLNDGQSWSQKRHYQEAYLNGHAET 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody 102 used for treating or preventing neuro-degenerative diseases - associated with proteins containing long poly:glutamine Example 7; Fig 7; 69pp; French.

The invention relates to a monoclonal antibody (MAb) 1C2 for the
                                     Score 202; DB 27; Length 870;
Pred. No. 8.55e-05;
81; Mismatches 128; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "putative translation initiation site"
86..107
/note= "polyglutamine region"
                                                                                                                                                                                                                                                                                                                                                                                                                                       305 ggyrm-lakhggyvwletggtviynprnlgpgcimcvnyvlse 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  331 PVYRFSLA-DGTIVTAQTKSKLFRNPVTNDRHGFVSTHFLQRE 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAY 1997.
08-NOV-1995; F01773.
08-NOV-1995; FF-013576.
(CNRS ) CNRS CENT NAT RECH SCI.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
LUZ X, MANGAL J, TOTA L, Trottier Y;
NPSDB; T78912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .r 15
W24800 standard; Protein; 914 AA.
                                       2.18;
                                                           Local Similarity 20.8%;
nes 59; Conservative
870 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9717445-A1.
Sequence
                                     Query Match
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                                                                            Matches
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cc suffering from spinocerebellar ataxia (SCA), with WAb 1C2 isolated 6

new sequences (178906-178911) encoding polyglutamine repeats. MAb 1C2

cc also isolated the complete SCA2 gene in clone DAN1 which appears to

cc contain 2 open reading frames (ORF), the second of which may be generated

cc contain 2 open reading frames (ORF), the second of which may be generated

cc contain a 22 amino acid polyglutamine region. Normal SCA2 proteins

cc contain 17-29 glutamines in the repeat whereas the mutant sequence

from patients with SCA contains at least 30, preferably 37-50 repeats.

cc from patients with SCA contains at least 30, preferably 37-50 repeats.

cc from patients with SCA contains at least 10, preferably 37-50 repeats.

cc from patients with scandard from the repeat whereas the mutant sequence

from patients with SCA contains at least 30, preferably 37-50 repeats.

cc from patients with scandard from nucleic acids encoding it are

specifically used to treat Huntington's disease, SCA types 1-5 or 7,

x-linked spino-bulbular muscular atrophy (Rennedy disease),

dentarorubral-pallidolusial atrophy, dominant autosomal spinocerebellar

cc ataxia familial spastic paraplegia, bipolar affective disorder, manic

cc ataxia familial spastic paraplegia, bipolar affective disorder, manic

Sequence 914 AA;

Query Match 2.1%; Score 203; DB 25; Length 914; Best Local Similarity 53.4%; Pred. No. 7.33e-05; Matches 31; Conservative 13; Mismatches 13; Indels 1; Gaps

ä

Search completed: Fri Sep 17 21:06:34 1999 Job time : 241 secs.

*****	(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm Fri Sep 17 21:16:43 1999; MasPar time 16.36 Seconds 878.195 Million cell updates/sec MPsrch_pp

Tabular output not generated.

>US-09-041-994-2 (1-1415) from US09041994.pep 9849 1 MSGLGENLDPLASDSRKRKL.......MNMNPMPMSGMPMGPDQKYC 1415

Title: Description: Perfect Score: Sequence:

PAM 150 Gap 11 Scoring table:

106580 segs, 10152877 residues Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1 Database:

Mean 36.592; Variance 199.242; scale 0.184

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	_		di			SUMMAKIES		
	sult No.	Score	Query Match	Query Match Length DB	DB	ID	Description	Pred. No.
'	-	232	2.4	848	;	US-08-366-	Sequence 4, Applicatio	1.87e-07
	7	232	2.4	848	Н	US-08-045-	4	1.87e-07
	e	235	.2.4	855	~	US-08-816-	7	1.16e-07
	4	231	2.3	802	H	US-08-366-	~	2.19e-07
	'n	231	2.3	802	Н	US-08-045-	7	2.19e-07
	9	210	2.1	360	~	US-08-531-	7	6.09e-06
	7	209	2.1	594	~	US-08-785-	é	7.13e-06
	ω	202	2.1	870	Н	us-08-785-	4	2.13e-05
	σ	210	2.1	2414	m	PCT-US95-0	~	6.09e-06
	10	210	2.1	2414	Н	US-08-227-	7	6.09e-06
	11	205	2.1	2441	~	US-08-194-	7	1.34e-05
	12	204	2.1	3144	Н	US-08-246-	ý	1.56e-05
	13	204	2.1		н	US-08-453-	6,	1.56e-05
	14	204	2.1	٣	7	US-08-457-	42,	1.56e-05
	15	197	2.0		7	US-08-185-	'n	4.65e-05
	16	199	2.0		7	us-08-185-	'n,	3.41e-05
	17	197	2.0		~	US-08-185-	4	4.65e-05
	18	197	2.0		7	US-08-185-	'n	4.65e-05
	19	193	7.0	788	~	US-08-918-	4,	8.66e-05
	50	194	2.0		~	us-08-267-	o,	7.41e-05
	71	200	7.0	875	Н	us-08-185-	Sequence 5, Applicatio	2.92e-05
	22	189	1.9	37	m	PCT-US96-1	Sequence 3, Applicatio	1.61e-04
	23	189	1.9	373	7	US-08-480-	Sequence 3, Applicatio	1.61e-04

sequence 3, Applicatio 4.05e-04 sequence 4, Applicatio 1.61e-04 sequence 7, Applicatio 1.61e-04 sequence 5, Applicatio 1.18e-04 sequence 52, Applicatio 1.38e-04 sequence 7, Applicatio 1.38e-04 sequence 7, Applicatio 1.38e-04 sequence 2, Applicatio 1.61e-04 sequence 2, Applicatio 1.61e-04 sequence 6, Applicatio 1.61e-04 sequence 13, Applicatio 1.60e-03 sequence 13, Applicatio 1.60e-03 sequence 13, Applicatio 1.60e-03 sequence 13, Applicatio 1.60e-03 sequence 51, Applicatio 1.32e-03 sequence 2, Applicatio 6.23e-03 sequence 2, Applicatio 1.32e-02	848 AA.	Ther A. Colls for Detecting Agonists to the Ah Loganus & Chestnut Me, Suite 960 Colls for Detecting Agonists to the Ah Loganus & Chestnut Me, Suite 960 Me, Suite 960 Me, Suite 960 Mersion #1.25 Median #1.25
24 183 1.9 678 3 PCT-US93-0 25 189 1.9 805 3 PCT-US96-1 27 191 1.9 805 2 US-08-480- 28 190 1.9 816 2 US-08-785- 30 183 1.9 816 2 US-08-785- 31 183 1.9 824 2 US-08-785- 32 189 1.9 826 2 US-08-785- 34 189 1.9 826 1 US-08-785- 35 174 1.8 542 1 US-08-785- 36 174 1.8 542 1 US-08-785- 37 174 1.8 542 1 US-08-284- 38 177 1.8 542 1 US-08-284- 40 178 1.8 542 1 US-08-284- 41 177 1.8 542 1 US-08-284- 42 163 1.7 521 3 PCT-US92-1 43 163 1.7 521 3 PCT-US92-1 44 165 1.7 521 3 US-08-185- 45 160 1 US-08-185- 46 1 177 1.8 742 1 US-08-190- 47 1 167 1.7 521 3 US-08-185- 48 165 1.7 755 1 US-08-190- 49 165 1.7 755 1 US-08-190-	RESULT 1 ID US-08-366-051B-4 STANDARD; PRT XX XX AC XXXXXX DT XX DT XX XX DT XX	No. 5630283 Linformation US/08366053 No. 5630283 Linformation: ICANT: Bradfield, Christopl ICANT: Carver, Lucy A. E OF INVENTION: Bahineered E OF INVENTION: Receptor E OF INVENTION: Bahineered E E OF INVENTION: Bahineered ATE: Illinois UNTRY: USA PURCHER: Bah PC compatible ERATION SYSTEM: PC-DOS/MS-I ENTARE: PATENTIN Release #1 ENTARE: PATENTION DATA: ENTRY APPLICATION DATA: ENTRY APPLICATION DATA: ENTRY APPLICATION DATA: ENTRY AGENT INFORMATION: WE: TILLON, THMOTHY L. COMMUNICATION INFORMATION: WE: TILLON, THMOTHY L. COMMUNICATION INFORMATION: ASSISTANTION SEQ ID NO: 4: EBENER CHARACTERISTICS: ATION FOR SEQ ID NO: 4: ENUE CHARACTERISTICS: NOTH: MAIN AND ACIDS POLUCGY: Linear

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97 -RQD--WK-PTFLSNEEFTQLMLEALDGFFLAIMTDGSIIYVSESVTSLLEHLPSDLVDQ 152
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                     25 PGQGLTCSGEKRRREQESKYIEELAELISANLSDIDNFNVKPDKCAILKETVRQIK- 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAEGIKSNPSKRHRDRLNTELDRLASLLP--FPQ-DVIN-KLDKLSVLRLSVSYLRAKSF 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Gaps
                                                                  83 FDVALKSSPTERNGGQDNCRAANFREGLNLQE-GEFLLQALNGFVLVVTTDALVFYASST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 2.4%; Score 235; DB 2; Length 855; Best Local Similarity 27.7%; Pred. No. 1.16e-07; Matches 46; Conservative 48; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08816693A
Patent No. 5874241
GENERAL INFORMATION:
APPLICANT: Takahashi, Joseph S
APPLICANT: Turek, Fred W
APPLICANT: Turek, Fred W
TITLE OF INVENTION: Clock Gene and Gene Product
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153 SIFNFIPEGEHSEVYKILSTHLLESDSLTPEYLKSKNQLEFCCHML 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,693A
                                                                                                                                                                                                                                       855 AA
                                                                                                                                                        142 IQDYLGFQQSDVIHQSVYELIHTEDRAEFQRQL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5874241thrup, Thomas E
REGISTRATION NUMBER: 33,268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
TENCE 855 AA; 96392 MW; 3883435 CN;
                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Prudential Plaza, STREET: Lolicago
STATE: Illinois
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08816693A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5460
TELEPAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 855 amino acids amino acids
                                                                                                                                                                                                                                       STANDARD;
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US-08-816-693A-2
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                                                                원
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Patent No. 5378822
GENERAL INFORMATION:
APPLICANT: Braditeld, Christopher Alan
APPLICANT: Dolwick, Kristin Marie
APPLICANT: Poland, Alan
TITLE OF INVENTION: Ah Receptor cDNA and Method of
TITLE OF INVENTION: Determining Human Risks To Environmental Pollutants
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADRESS:
                                                                                  7;
                                                                                                                                                                                    83 FDVALKSSPIERNGGQDNCRAANFREGLNLQE-GEFLLQALNGFVLVVTIDALVFYASST 141
                                                                                                                                                                                                        25 PGQGLTCSGEKRRREQESKYIEELAELISANLSDIDNFNVKPDKCAILKETVRQIRQIK- 83
                                                                                                                  27 PAEGIKSNPSKRHRDRLNTELDRLASLLP--FPQ-DVIN-KLDKLSVLRLSVSYLRAKSF 82
                                                                                    Gaps
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                                               Query Match 2.4%; Score 232; DB 1; Length 848; Best Local Similarity 27.5%; Pred. No. 1.87e-07; Matches 42; Conservative 52; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TERE FLORM:
MEDIUM TERE FLORPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATE FLORE
COMPAGE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: 19390408
FLING DATE: 19390408
FLING DATE: 19390408
TLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Fentress, Susan B.
REGISTRATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-9207
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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STREET: 100 South Wacker Drive, Suite 960
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                                                                                                                                                                                                                                                                                                                                                           848
                                                                                                                                                                                                                                                  142 IQDYLGFQQSDVIHQSYYELIHTEDRAEFQRQL 174 ::|| ::|| ::|| ::| | :|| 141 VTQYLQYKQEDLVNTSVYNILHEEDRKDFLKNL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
PENCE 848 AA; 96113 MW; 3734382 CN;
MOLECULE TYPE: protein
SEQUENCE 848 AA; 96113 MW; 3734382 CN;
                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/08045806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (312-456-7776
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
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AMINO ACID
                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RY: USA
60606-4002
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US-08-045-806-4
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RESULT

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Sequence 2, Application US/08045806
Patent No. 5378822
CEREAL INFORMATION:
CENTRAL TROUBATION:
CENTRAL TITLE OF INVENTION:
CENTRAL TELE OF INVENTION:
CENTRAL TELES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82 FDVALKSTPADRNGGQDQCRAQ-IRDWQDLQEGEFLLQALNGFVLVVTADALVFYASSTI 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
FENCE 805 AA; 90351 MW; 3331614 CN;
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                                                                                                                         Sequence 2, Application US/08045806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Fentress, Susan B.
REGISTATION NUMBER: 31,327
REFERENCE/DOCKET NUMBER: NU-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (312)-456-8000
TELEFAX: (312)-456-7776
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 805 amino acids
AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bradfield, Christopher A.
APPLICANT: Dolwick, Kristin M.
APPLICANT: Carver, Lucy A.
ATILE OF INVENTION: A. Receptor cDNAs and Genetically
TITLE OF INVENTION: Engineered Cells for Detecting Agonists to the Ah
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 36
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
STREET: 100 South Wacker Drive, Suite 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 FDVALKSTPADRNGGQDQCRAQ-IRDWQDLQEGEFLLQALNGFVLVVTADALVFYASSTI 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Best Local Similarity 30.3%; Pred. No. 2.19e-07;
Matches 46; Conservative 46; Mismatches 52; Indels
156 SYYNILHEEDRKDFLKNLPKSTYNGVSWTNEPQRQKSH-TFNCRML 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 6066-4002
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/366,051B
                                                                                                                       805 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            805 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|| : | | | : : | | | : : | | | : | | | 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
JENCE 805 AA; 90351 MW; 3331614 CN;
                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08366051B
Patent No. 5650283
                                                                                                                                                                                                                                                                  Sequence 2, Application US/08366051B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Tilton, Timothy L.
REGISTRATION NUMBER: 16,26
REFERENCE/DOCKET NUMBER: NU-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (312)-456-8000
TELEFAX: (312)-456-776
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 805 amino acids
TYPE: amino acid
                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
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                                                                                                US-08-366-051B-2
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ID US-08-045-806-2
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268 BUSH STREET, SUITE 3200
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COMPUTER READABLE FORM:
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AC XXXXXX
AC XXXXXX
DT XX
DT XX
C Sequence 4, Applic
XX Sequence 4, Applic
XX Sequence 4, Applic
XX Sequence 7, Applic
XX S
                                                                                                     COUNTRY: UZIP: 94104
                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 AFR 242
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                                                                                         APPLICANT: Kakluka, Akira
TITLE OF INVENTION: DNA Sequence Encoding the Machado-Joseph
Patent No. 5840491
TITLE OF INVENTION: Disease Gene and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
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                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,927B
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
PROOR APPLICATION NUMBER: DP H6-251600
FILING DATE: 21-SEP-1994
ATTONREY/AGENT INPORMATION:
AND APPLICATION NUMBER: DP H6-251600
FILING DATE: 21-SEP-1994
ATTONREY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Patent No. 5840532
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MCKNIGht, Steven L.
APPLICANT: Russell, David W.
TITLE OF INVENTION: Neuronal PAS Domain Protein NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 2.1%; Score 210; DB 2; Le Best Local Similarity 44.4%; Pred. No. 6.09e-06; Matches 40; Conservative 14; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              594 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288 YFEKQQQKQQQQQQQQQQQQQQQQQQQQQQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
ENCE 360 AA; 41531 MW; 592461 CN;
Sequence 2, Application US/08531927B
Patent No. 5840491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/08785310A
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                                                                                                                                                                                                                                                                                                                                  CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 02173-4799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-785-310A-6
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123 RRGPVALVSE-VFEQH-LGGHILQSLDGFVFALNQEGKFLYISETVSIYLGLSQVELTGS 180
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Patent No. 5695963
GENERAL INFORMATION:
APPLICANT: RUSSell, David W.
APPLICANT: Tien, Hu!
TITLE OF INVENTION: Endothelial PAS Domain Protein
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 209; DB 2; Length 594; Pred. No. 7.13e-06; 35; Mismatches 50; Indels
                                                                                             COMPUTE: FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ENDAPY disk
COMPUTER: ENDAPY disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: D3.008/785,310A
FILING DATE: 21-JAN-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 34,434
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 594 antino acids
TYPE: amino acids
TYPE: amino acids
TYPE: ATRADEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
FENCE 594 AA; 63736 MW; 1871071 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08785241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
2.1%;
Best Local Similarity 28.5%;
Matches 35; Conservative
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CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
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1025 ONRPLERNSLDDLVGPPSNLEGOSD-ERALLDQLHTLLSNTDATGLEEIDRALGIPE-LV 1082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1950 RPIQHQMPPMTPMAPMGMNPPPMTRGPSGHLEPGMGPTGMQQQPPWSQGGLPQPQLQSG 2009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2010 MPRPAMM-SVAQH-GQPLNMAPQPGLGQVGISPLKP--GTVSQQALQNLLRTLRSPSSPL 2065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1256 QQQQQQQQQQQQTQAFSPPPNVTASPSMDGLLAGPTMPQAPPQQFPYQPNYGMGQQPDPA 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2066 QQQQVL-SILHA-NPQLLAAFIKQRAAKYANSNP-QPIPGQPGMP-QGQ-PGLQPPTMPG
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                                                                                                                                                                                                                                                                                                                                                                                     Score 210; DB 3; Length 2414;
Pred. No. 6.09e-06;
91; Mismatches 167; Indels 35;
 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                            FILING DATE.
CLASIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,536
FILING DATE: 14-April-1994
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Holliday C. Heine, Ph.D.
REGISTATION NUMBER: 34,346
REFERENCE/DOCKET NUMBER: DFI-198Xq
TELECOMMUNICATION INFORMATION:
TELEFONE: (617) 642-2290
TELEFAX: (617) 451-0313
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
FUNCTH: 2414 amino acids
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
SEQUENCE 2414 AA; 264143 MW; 29411911 CN;
                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04682
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Patent No. 5658784
GENERAL INFORMATION:
APPLICANT: Eckner, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/08227536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Eckner, Richard
APPLICANT: Ewen, Mark
APPLICANT: Livingston, David
                                                                                                                                                                                                                                                                                             : 2414 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                     y Match 2.1%;
Local Similarity 25.6%;
hes 101; Conservative
                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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Pred. No. 2.13e-05;
81; Mismatches 128; Indels 15; Gaps 14;
                                                                                                                                                                                                                                                                                                                                                                                                                    71 SSVCSENESEAEADQQMDNLYLKALEGFIAVVTQDGDMIFLSENISKFMGLTQVELTGHS 130
                                                                                                                                                                                                                                                                                                                                                                                                                                98 ADVSSTGGGVIDKDS-LGPLLLQALDGFLFVVNREANIVFVSENVTQYLQYKQEDLVNTS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 VYNILHEEDRKDFLKNLPKSTVNGVSWTNEPQRQKSHTFNCRML-MKTPHDILEDINASP 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 IFDFTHPCDHEEIRENLSLKNGSGFG-KKSKDMSTERDFFWRWKCTVTNRGRTVNLKSAT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 MDMKFTYCD-DRI-TELI-GYHPEELLGRSAYEFYHALDSEN-MTKSH-QNLCTKGQVVS 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 LSGKVVNIDTNSLRSSMRPGF--EDIIRRCIQRFFSLNDGQSWSQKRHYQEAYLNGHAET 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190 WKVLHCTGQVKVYNNCPPHNSLCGYKEPLLSCLIIMCEPIQHPSHMDIPLDSKTFLSRHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
TITLE OF INVENTION: NUCLEIC ACID ENCODING TRANSCRIPTION
TITLE OF INVENTION: FACTOR P300 AND USES OF P300
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weingarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305 GOYRM-LAKHGGYVWLETQGTVIYNPRNLQPQCIMCVNYVLSE 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA.
                                                                                                   ATTORNEY/AGENT INPORTATION:
NAME: OSMAN, RICHARD A
REGISTARION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UTSD:1229
TELECOMMUNICATION INPORMATION:
TELEPONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 870 mnino acids
                                                        APPLICATION NUMBER: US/08/785,241
FILING DATE: 17-JAN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
ENCE 870 AA; 96516 MW; 4016567 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                       Query Match 2.1%;
Best Local Similarity 20.8%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: MA
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RY: US
02109
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PCT-US95-04682-2
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Sequence 2, Application US/08194468
Patent No. 5750336
GENERAL INFORMATION:
APPLICANT: Montminy, Marc R.
TITLE OF INVENTION: COMPOUNDS WHICH INHIBIT ACTIVATION OF TITLE OF INVENTION: RESPONSIVE GENES
NUMBER OF SEQUENCES: 3
CORRESPONDED ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
SEQUENCE 2441 AA; 265473 MW; 30223014 CN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US/08/194,468
10-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY, CASE AT SECTION TO SECT
                                 Sequence 2, Application US/08194468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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Local Similarity 29.4%;
les 65; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JT 12
US-08-246-982A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1950 RPIQHQMPPMTPMAPMGMNPPPMTRGPSGHLEPGMGPTGMQQQPPWSQGGLPQPQQLQSG 2009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2010 MPRPAMM-SVAQH-GQPLNMAPQPGLGQVGISPLKP--GTVSQQALQNLLRTLRSPSSPL 2065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2066 QQQQVL-SILHA-NPQLLAAFIKQRAAKYANSNP-QPIPGQPGMP-QGQ-PGLQPPTMPG 2120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2234 MOGGNMGOIGQLPQALGAEAGASLQAYQQRLLQOQMGSPVQPNPMSPQQHMLPNQAQSPH 2293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1025 ONRPLIRNSLDDLVGPPSNLEGQSD-ERALLDQLHTLLSNTDATGLEEIDRALGIPE-LV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2176 PSQFRDILRRQQMMQQQQQGAGPGIGP-GMAN-HNQFQQPQGVGYPPQPQQRMQHHMQQ
     NUCLEIC ACID, ENCODING TRANSCRIPTION FACTOR P300 AND USES OF P300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.1%; Score 210; DB 1; Length 2414; Local Similarity 25.6%; Pred. No. 6.09e-06; les 101; Conservative 91; Mismatches 167; Indels 33
TITLE OF INVENTION: NUCLEIC ACID, ENCODING TRANSCRII
TITLE OF INVENTION: FACTOR P300 AND USES OF P300
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Welnqarten, Schurgin, Gagnebin & Hayes
STREET: Ten Post Office Square
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/227,536
FILING DATE: 14-APR-1994
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2441 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT INFORMATION:

NAME: Williams Ph.D., Kathleen A.

REGISTRATION UNBER: 34.380

REFERENCE/DOCKET NUMBER: DFCI-308XX

TELEPHONE: (617) 542-2290

TELEPHONE: (617) 542-2290

TELEFAX: (617) 542-2290

TELEFAX: (617) 451-0313

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2414 amino acids

TYPE: amino acid

TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2294 LQGQQIPNSLSNQVRSPQPVPSPRPQSQPPHSSP, 2327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
FINCE 2414 AA; 264143 MW; 29411911 CN;
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                                                                                                                                                                                        STATE: MA
COUNTRY: U
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US-08-194-468-2
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2116 MQPQPGLQSQPGMQPQPGMHQQPSL-QNLNAMQAGVPRPGVPPPQPAMGGLNPQGQALNI 2174
                                                                                                                                                                          2232 QOPGGFGGYA-PAMQQQRMQQHLPIQGS-SMGQMAAP-MGQLG---Q-MGQPGLGADSTP 2284
                                                                                                                                                                                            1279 ASPSMDGLLAGPIMPQAP-PQQFPYQPNYGMGQQPDPAFGRVSSPPNAMMSSRMGPSQNP 1337
                               Gaps
                               Indels 14;
 Length 2441;
                                                                                                                                                                                                                                   2285 NIQQALQQRILQQQQMKQ-QIGSPGQPNPMSPQQHMLSGQP 2324
                                                                                                                                                                                                                                                    3144 AA
Score 205; DB 2; Le:
Pred. No. 1.34e-05;
45; Mismatches 97;
                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08246982A
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SEQUENCE
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 888888888888888888888888888888
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Patent No. 5693757
GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: MacDonald, Marcy E.
APPLICANT: Ambrose, Christine M.
APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1110 New York Avenue
                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                              Query Match 2.1%; Score 204; DB 1; Length 3144; Best Local Similarity 54.2%; Pred. No. 1.56e-05; Matches 32; Conservative 8; Mismatches 18; Indels
                                                                                                                  COUNTRY U.S.A.

21P: 2005

21P: 2005

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILING DATE: MAY 20, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/POCKET NUMBER: 29,021
REFERENCE/POCKET NUMBER: 29,021
REFERENCE/POCKET NUMBER: (2009) 3880002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                      MLE TYPE: protein
3144 AA; 347896 MW; 52186077 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08453265
                                                                                                                                                                                                                                                                             TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         3144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                  CITY: Washington STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: D.C. COUNTRY: U.S.A. ZIP: 20005
Patent No. 5686288
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-453-265-6
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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APPLICANT: Hayden, Michael
APPLICANT: Lin, Biaoyang
APPLICANT: Lin, Biaoyang
APPLICANT: Nasir, Jamal
TITLE OF INVENTION: Mouse Model for Huntington's Disease and
TITLE OF INVENTION: Related DNA Sequences
TITLE OF INVENTION: Related DNA Sequences
AURESPONDENCE: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Virginia Bennett
STREET: PO Box 37428
CITY: Raleigh
STATE: No. 5849995th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.1%; Score 204; DB 1; Length 3144;
Best Local Similarity 54.2%; Pred. No. 1.56e-05;
Matches 32; Conservative 8; Mismatches 18; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: R. LOPPY ULS.

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LUDWIG, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 36,203
TELECOMMUNICATION INFORMATION:
TELEFRONE: (202) 371-2600
TELEFRA: (202) 371-2500
TELEFRA: (202) 371-2500
TELEFRA: (202) 371-250
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 3144 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
JENCE 3144 AA; 347896 MW; 52186077 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,273B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 42, Application US/08457273B Patent No. 5849995 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 27627
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 42, Application US/08457273B
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ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Virginia C.
REGISTRATION NUMBER: 37,092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 34
FELECOMMUNICATION INFORMATION:
TELEPHONE: 919-854-1400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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ADDRESSEE: PENNIE & EDMONDS STREET: 1155 Avenue of the Americas CITY: New York STATE: New York STATE: New York COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: Isabelle FORM: MEDIUM TYPE: Floppy disk COMPUTER: EISPPY DISK STREET: DISK STEET: DISK STEET: DISK COMPUTER: DISK STEET: DISK COMPUTER: DISK STEET: DISK ST
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                                                                                                                                                                                                                                                                                                                      20 QQQQQQQQQQQQQQQQQQQQQPPPPPPQLPQPPPQAQPLLPQPQPPPPPPP 78
                                                                                                                                                                                                                             Query Match 2.1%; Score 204; DB 2; Length 3144; Best Local Similarity 54.2%; Pred. No. 1.56e-05; Matches 32; Conservative 8; Mismatches 18; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08185432
Patent No. 7550652
GENERAL INFORMATION:
APPLICANT: Artavanis-Tsakonas, Spyridon
                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
FENCE 3144 AA; 347856 MW; 52223419 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
ENCE 303 AA; 33746 MW; 451837 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08185432
                       42:
TELEFAX: 919-854-1401
INFORMATION FOR SEQ ID NO: 42
SEQUENCE CHARACTERISICS:
LENGTH: 3144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 303 amino acids
TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                    TYPE: amino acid
STRANDEDNESS: single
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US-08-185-432-5
                                                                                                                                                                                  SEQUENCE
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 Db
 273 QQQQHHHQHQQQQQHQQQQQHQMQ 295

y 1247 QQQQQQQQQQQQQQQQQTQ 1269

Search completed: Fri Sep 17 21:17:45 1999 Job time : 62 secs.

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2 4451.6
                                                   September 17, 1999, 19:18:26; Search time 1821.02 Seconds (without alignments) 7852.012 Million cell updates/sec
                                                                                               1 GCTGGATGGTGGACTCAGAG......CATTTGAGCAGGAATTCTAG 4496
       GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd.
                                                                                                                             679419 seqs, 1590154680 residues
                                     OM nucleic - nucleic search, using sw model
                                                                                 US-09-041-994-1
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gb_htg2:*
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em_htg: *
em_hum1: *
em_hum2: *
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em_bal:*
em_ba2:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8 Score Match Length DB ID Description	AF010227 Homo sapi
ID	1 4468.2 99.4 4495 11 AF010227
DB	11
Length	4495
% Query Match	99.4
sult Query No. Score Match Length DB ID	4468.2
Result No.	7

AF012108 Homo sapi AF03683 Homo sapi AF036892 Homo sapi AF00581 Mus muscu AF044080 Xenopus 1 AL034418 Human DNA U80737 Homo sapien X97674 H.sapiens m U39060 Mus musculu AF136943 Rattus no AF000882 Homo sapi AJ000882 Homo sapi AJ000882 Human stero U59302 Human stero U59302 Human stero U56428 Mus musculu U56920 Mus musculu	human S human S human TA Human TA Homo sa Homo sa Homo S Homo S Homo S Homo S Sequen S Sequen		13-AUG-1997 r 3 (RAC3) mRNA, tebrata; Mammalia; Homo. 1 coactivator that is 1-8484 (1997) lecular Toxicology, 55 Lake Avenue North,
AF012108 AF016031 AF036892 AF036892 AF04080 HS1049516 HSTEG0737 HSTEG0737 AF139060 AF000881 HSJ000881 HSJ000881 HSJ000882 HSJ000882 MMU56920 MMU56920	G09716 G09672 G09672 G1967161 UMTF11D HUMMF11DA AF071309 AF117755 AF117755 AF117755 AF117755 AF117755 AF072263	AUJZA 65 KUJZA 65 HSTFI IDAA MACATSI MACATSI MACATSI DAT 16899 DAT 16899 MSQRTIRET RNUB7960 SMN1	mRNA PRI associated coactivato ordata; Craniata; Ver tarrhini; Hominidae; I receptor-associated IF2 U.S.A. 94 (16), 8479 omes, P.J.) Pharmacology and Mc setts Medical School,
		0000 0000	95; 33; 38; 38; 38; 38; 38; 38; 38; 38; 38
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                                                                                                                                                                                                                                                                                                     /note-"transcriptional coactivator with intrinsic->histone acetyltransferase activity; member of the steroid/nuclear receptor-associated coactivator family which includes steroid receptor coactivator [SRC-11), transcriptional intermediate factor 2 (TIF2), and receptor associated coactivator 3; similar to the mouse p300/CBP/co-integrator protein (p/CIP) and the activator of retinoid receptors (ACIP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"receptor-associated coactivator 3"
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99.8%; Pred. No. 0;
ive 0; Mismatches
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/cell_line="HeLa"
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Location/Qualifiers
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Matches 4486; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6835)

Anzick,S.L., Krononen,J., Walker,R.L., Azorsa,D.O., Tanner,M.W., Guan,X.Y., Sauter,G., Kallioniemi,O.P., Trent,J.M. and Meltzer,P.S. AIBI, a steroid receptor coactivator amplified in breast and science 277 (5328), 965-968 (1997)

Homo sapiens

human.

SOURCE

REFERENCE AUTHORS National

ry of Cancer Genetics, Nation 49 Convent Dr., Bethesda, 1

Anzick, S.L., Walker, R.L., Guan, X.-Y. and Meltzer, P.S. Direct Submission
Submitted (01-JUL-1997) Laboratory of Cancer Genetics Human Genome Research Institute, 49 Convent Dr., Beth

2 (bases 1 to 6835)

AUTHORS TITLE JOURNAL

JOURNAL MEDLINE REFERENCE

TITLE

/organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="20" //map="20q12"

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Location/Qualifiers

20892-4470,

FEATURES

1. .6835 USA

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/translation="MSGLGENLDPLASDSRKRKLPCDTPGQGLTCSGEKRRREQESKY
IEELAELISANLSDIDNFNVKPDKCAILKETVRQIRQIKEQGKTISNDDDVQKADVSS
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RNSLDDLVGPPSNLEGGSDERALLDOLHTLLSNTDAYGLEEIDRALGIPELVOGGOAL
EPKQDAFQGQEAAVMMDQKAGLYGQTYPAQGPPWQGGFHLQGGSPSFNSMMNQMNQOG
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                                                                                                                                                                                       /note="nuclear receptor co-activator"
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/protein_id="AAC51677.1"
/db_xref="PID:92331250"
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                                            /gene="AIB1"
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6835 bp mRNA PRI 21-AUG-1997 Amplified in Breast Cancer (AIBI) mRNA, complete cds.

GI:2331249

Homo sapiens A AF012108 92331249 AF012108.1 GI AF012108

DEFINITION ACCESSION

KEYWORDS, VERSION

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RESULT : AF012108 LOCUS

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oy Db	301	aaaggaaacagtaagacagatacgtcaataaaagagcaaggaaaaactatttccaatga 360 	
	361	TGATGATGATCAAAAAGCCGATGTATCTTCTACAGGGCAGGGAGTTATTGATAAAGACTC 420 	
O _Y	421	CTTAGGACCGCTTTTACTTCAGGCATTGGATGGTTTCCTATTGTGGTGAATCGAGAGGC 480 	
Oy Dp	481	AAACATIGTATTIGTATCAGAAAAIGTCACACAATACCIGCAATATAAGCAAGAGGACCT 540 	
oy og	541 656	GGTTAACACAAGTGTTTACAATATCTTACATGAAGAGAGAG	
9	601	TTTACCAAAATCTACAGTTAATGGAGTTTCCTGGACAAATGAGCCCCAAAGACAAAAAG 660 	
Oy Dp	661	CCATACATTTAATTGCCGTATGTTGATGAAAACACCACATGATATTCTGGAAGACATAAA 720 	
Oý Pp	721	CGCCAGTCCTGAAATGCGCCAGAGATATGAAACAATGCAGTGCTTTGCCCTGTCTCAGCC 780 	
ò	781 896	ACGAGCTATGATGGAGGAAGGGGAAGATTTGCAATCTTGTATGATCTGTGTGGGCACGCCG 840	
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ç, Op	901	TCTTTCAGGAAAGGTGTCAATATAGATACAAATTCACTGAGATCCTCCATGAGGCCTGG 960 	
O.Y.	961	CTTTGAAGATATAATCCGAAGGTGTATTCAGAGATTTTTAGTCTAAATGATGGGCAGTC 1020 	
Oy Dp	1021	ATGGTCCCAGAAACGTCACTATCAAGAAGCTTATCTTAATGGCCATGCAGAAACCCCAGT 1080 	
OY Db	1081	ATATCGATTCTCGTTGGCTGATGGAACTATAGTGACTGCACAGAAAAAGCAAAACTCTT 1140 	
Oy Dp	1141	CCGAAATCCTGTAACAAATGATCGACATGGCTTTGTCTCAACCCACTTCCTTC	

GAGCAGCAGGCCTATGGCTTGGCAGACCCTAGCACCACAGGGCCAGATGAGTGGAGCTAG TACTGGGAACCACAGCTTTCCAGCAGCTCTCTCAGTGCCCTGCAAGCCATCAGTGGAAGG GAATTCACCAGCTGAGGTAGCCAAGATTACTGCACAAGCCACTGGGAAAGACACACGGGG GAATICACCAGCIGAGGIAGCCAAGATIACIGCAGAAGCCACIGGGAAAGACACCAGCAG TGGATGCAACAGTTCGGTAGGCGGCATGAGTATGTCGCCAAACCAAGGCTTACAGATGCC CAATATGAATATTACCCAACCAAGTAAAGTAAAGCAATCAGGATTCCAAGAGTCCTCTGGG GGAGAATAATGCACTTCTTAGATACCTGCTGGACAGGGATGATCCTAGTGATGCACTCTC 9 g g 셤 δ g 8 8 8 9 9 δ g ò ద οy g ద 셤 요 g 8 8 à 셤 ò 원 à ò õ ò à à ò ·δ

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Takeshita, A., Cardona, G.R., Koibuchi, N. and Chin, W.W.
Direct Submission
Submitted (24-JUJ-1997) Medicine, Brigham and Women's Hospital,
Harvard Medical School, 20 Shattuck Street #905, Boston, MA 02115,
USA
                                                                                                                                                     AF016031 4668 bp mRNA PRI 05-NOV-1997
Homo sapiens thyroid hormone receptor activator molecule (TRAM-1)
mRNA, complete cds.
AF016031
92584879
AF016031.1 GI:2584879
                                                                                                                                                                                                                                                                                                                                                                                                                              Takeshita, A., Cardona, G.R., Kolbuchi, N., Suen, C.S. and Chin, W.W. TRAM-1, A novel 160-kDa thyroid hormone receptor activator molecule, exhibits distinct properties from steroid receptor
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4668)
Takeshita, A., Cardona, G.R., Kolbuchi, N., Suen, C.S. and Chin, W
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0; Mismatches
98.5%;
99.2%;
Query Match 98.5
Best Local Similarity 99.2
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අ	1247	ATCCTGTAACAAATGATCGACATGGCTTTGTCTCAACCCACTTCCTTC
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KYETMQCFALLQPRAMBEGEBLQSCMICVARRITTGERTPFDNIPESTTRHDLSGK
VVNIDTNSLRSSMRPGEIIRRCIQRFFSLNDGQSWSQKRHYQEVTSDGIFSPTAYL
NGHAETPVTRSLADGTIVTAQTKSKLERNEVTNDRHGEVSTHFLQRRQNGYRDNPUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expression Lab, The Salk Institute for Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6754)

Chen, H., Lin, R.J., Schiltz, R.L., Chakravarti, D., Nash, A., Nagy, L., Privalsky, M.L., Nakatani, Y. and Evans, R.M.

Nuclear receptor coactivator ACTR is a novel histone acetyltransferase and forms a multimeric activation complex with P/CAF and CBP/p300

Cell 90 (3), 569-580 (1997)
                                                                                                                                                                                     4473
                                                                                                                                                                                                        (ACTR) mRNA, complete
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/note-"activator for thyroid hormone and retinoid
receptors; member of the nuclear receptor coactivator
family which includes SRC-1, TIF2/GRIP1; similar to
                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-1997
                                 GGTGCACATGAATGGCAGCAGTGGTCACATGGGACAGATGAACATGAACCCCATGCCCAT
                                                                                                                                                4414 CAGGCATCCATCTTGGAAGAAAGGACCAGCTTTGAGCTCCATCAAGGGTATTTTAAGTGA
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/protein_id="A8992388.1"
/db_xref="PlD:9270770"
/db_xref="G1:2707770"
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/codon_start=1
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/db_xref="taxon:9606"
/cell_type="leukocyte"
1. .6754
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Submitted (03-DEC-1997)
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en, H. and Evans, R.M.
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/gene="ACTR"
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oy B	1831 TTCAATGTGTCAGTCAAATAGCAGAGATCACCTCAGTGACAAAGAAAG	
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S S	/ 2371 GGACAATAAAATGAGTCGGTGCACCAGCTCCACCATTCCTAGCTCAAGTCAAGAAGA 2430	
ŏ	2431 CCCTAAAATTAAGACAGAGACAAGTGAAGAGGATCTGGAGACTTGGATAATCTAGATGC 2490 	
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S Torchia,J. and Rosenfeld,M.G.
Direct Submission

Direct Submission

Submitted (21-APR-1997) Medicine, Howard Hughes Medical Institute at the University of California, San Diego, 9500 Gilman Drive, C.M.M. 345, La Jolla, CA 92093-0648, USA

Torchia,J. and Rosenfeld,M.G.
Direct Submission

L Submitted (06-MR-1998) Medicine, Howard Hughes Medical Institute at the University of California, San Diego, 9500 Gilman Drive, C.M.M. 345, La Jolla, CA 92093-0648, USA
Sequence update by submitter
Sequence update by submitter
On Mar 6, 1998 this sequence version replaced 91:2213814.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 4609)
1 Torchia,J., Rose,D.W., Inostroza,J., Kamei,Y., Westin,S.,
Glass,C.K. and Rosenfeld,M.G.
The transcriptional co-activator p/CIP binds CBP and mediates nuclear-receptor function
Nature 387 (6634), 677-684 (1997)
                                                                                                                                                                                                                     4014 CCCCAGCATGGATGGGCTTTTGGCAGGACCCACAATGCCACAAGCTCCTCCGCAACAGTT
                                     4374 CATGCCCATGTCTGGCATGCCTATGGGTCCTGATCAGAAATACTGCTGACATCTCTGCAC
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                                                                      <u> ACACCCGCAGGCTGCATCTATCAGTCCTCAGAAATGAAGGGCTGGCCATCAGGAAA</u>
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RORYETMOCFALSOPRAMLEEGEDLOCCMICVARRYTAPFESSPESFITRHDLSGKVV
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                                                                                                                         /note="nuclear receptor coactivator protein; p/CIP'
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Best Local Similarity 78.9
Matches 3547; Conservative
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ි සි	445	CICITIAGGACCGCTITIACIACAGGCACIGGAIGGITICCIGITIGIGGIGAAICGAGA 504	
O O	478	GGCAAACAITGIAITIGIAITCAGAAAAIGICACACAAIACCIGCAAIAIAAGCAAGAGGA 537 	
oy g	538	CCTGGTTAACACAAGTGTTTACAATATCTTACATGAAGAGAGAAGGAAG	
o o	598 624	GAATITACCAAAAICIACAGITAAIGGAGITICCIGGACAAAIGAGCCCCAAAGACAAAA 657 	
S S	658 684	AAGCCATACATTTAATTGCCGTATGT-TGATGAAACACCACATGATATTCTGGAAGACA 716 	
	717	TAAACGCCAGTCCTGAAATGCGCCAGAGATATGAAACAATGCAGTGCTTTGCCCTGTCTC 776 	
Oy Db	777	AGCCACGAGCTATGATGGAGGAAGGGGAAGATTTGCAATCTTGTATGATCTGTGTGGGCAC 836	
9 8	837	GCCGCATTACTACAGGAGAAAGAACATTTCCATCAAACCCTGAGAGCTTTATTACCAGAC 896 	
Q Pp	897 915	AIGATCTITCAGGAAAGGIIGICAATAIAGAAAATICACIGAGAICCTCCAIGAGGC 956 	
Q Q	957 975	CIGGCITTGAAGATATAATCCGAAGGTGTATTCAGAGATTTTTTAGTCTAAATGATGGGC 1016 	
oy Op	1017	AGTCATGGTCCCAGAAACGTCACTATCAAGAAGCTTATCTTAATGGCCATGCAGAAACCC 1076 	
QY Db	1077	CAGTATATCGATTCTCGTTGGCTGATGGAACTATAGTGACCAGCAGAAAAAGCAAAC 1136 	
	1137	TCTTCCGAAATCCTGTAACAAATGATCGACATGGCTTTGTCTCAACCCACTTCCTTGAGA 1196 	
8 %	1197	GAGAACAGAATGGATATAGACCAAAACCCAAATCCTGTTGGACAAGGGATTAGACCACCTA 1256 	
Qy Dp	1257	TGGCTGGATGCAACAGTTCGGTAGGCGGCATGAGTATGTCGCCAAACCAAGGCTTACAGA 1316 	
Qy Dp	1317	TGCCGAGCAGCAGGGCCTATGGCTTGGCAGCCCTAGCACCACAGGGCAGATGAGTGGAG 1376 	
S S	1377	CTAGGTATGGGGGTTCCAGTAACATAGCTTCATTGACCTGGGCCAGGCATGCAATCAC 1436 	
ç q	1437	CATCTTCCTACCAGAACAACAATGGGCTCAACATGAGTAGCCCCCCACATGGGAGTC 1496 	
Q D	1497	CIGGICITGCCCCAAACCAGAATAICAIGAITICICCICGIAAICGIGGGAGICCA 1556 	

AGATAGCCTCACATCAGTTTTCTCCTGTTGCAGGTGTGCACTCTCCCATGGCATCTTCTG ACCGGGGTCATTCCTCCTTGACCAACTCCCCCTAGATTCAAGTTGTAAAGAATCTTCTG TCTCTAAAGAACTACAGCCCCAAGTGGAAGGAGTGGACAATAAAATGAGTCAGTGCACCA GCTCCACCATTCCTAGCTCAAGAGAAAGACCCTAAAATTAAGACAGAGACAAGTG AAGAGGGATCTGGAGACTTGGATAATCTAGATGCTATTCTTGGTGATCTGACTAGTTCTG ATCACCTCAGTGACAAAGAAAGTAAGGAGAGCAGTGTTGAGGGGGGCCAGAGAATCAAAGGG ACTITITACAAITAAITCCAITAICCICAAAIGGIAGICAICIGGGGACIAAGCAACAGGIGI TTCAAGGAACTAATTCTCTGGGTTTGAAAAGTTCACAGTCTGTGCAGTCTATTCGTCCTC 2277. g g QQ g g g g g g g 셤 δ g ò g ò 셤 à 셤 δ ద ò g ò g ò ò δ ò ò ογ ò à à

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                                               TGATGGATAGTCAGGAGAATTACGGTGCCAACATG---GGCCCAAACAGAAATGTTCCTG
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AF044080 4546 bp mRNA VRT 09-APR-1998 Xenopus laevis retinoid X receptor-interacting coactivator xSRC-3 mRNA, complete cds.
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AGCAGGGTTTTCTTAATGCTCAAATGGTCGCCCAACGCAGCAGAGAGCTGCTAAGTCATC
                                         CCCAGGCTTTCTTTAATGCCCAAATGGCTGCCCAGCAGAAACGAGAGCTGATGAGCCATC
                                                                       CACCTCCTAATGTGACTGCTTCCCCAGCATGGATGGCTTTTGGCAGGACCCACAATGC
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MHPRANLI PRINNI PKQLRMQLAQRLGGQGFLMQNRQALEMKVDPMNPGGAGVMRPVM
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TQMYPSPDMKGWPSGNMARPNSFPQQQYSHDPTGTNAMMSRNAMGGNHMGQMNINSLP
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Kim,H.-J., Lee,S.-K., Na,S.-Y., Choi,H.-S. and Lee,J.W.
Direct Submission
Submitted (22-JAN-1998) Pharmaceutical Sciences, Chonnam Univ., 300 Yongbong-dong Puk-ku, Kwangju 500-757, Korea Location/Qualifiers
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 CAGGCATIGGAIGGTITCCIATITGIGGIGAAICGAGAGGCAAACAIIGIAITIGIAICA 499
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2470 1848 1999 2119 2019 2079 2290 2199 2410 2379 1579 TCCAGCAGCTCTCTCAGTGCCCTGCAAGCCATCAGTGAAGGTGTGGGGGACTTCCCTTTA TCTACTCTGTCATCACCAGCCCCAAATTGGATAACTCTCCCAATATGAATATTACCCAA 1609 TCATCATTATCTTCTCTGGCCAGAAGTAGAGAACAATTCCAATATGAACATGCCCCAG 1669 CAGGGTAAAATTTGCAACCAGGATTGTAAGAGTCCCAGTGGCTTGTACTGTGAACAAGGA 1729 CAAGTGGAAAGCTCTGTGTCAGTCAAGCGGTAGGGAGCACCTTGGTGAAAAAAGACGTT **AAAGAGAACATATTTGAAGGGTCGGAGAGTCAGAGATCACAAGCTGAAAGTAAAGGGCAT** AACTCCCCCCTAGATTCAAGTTGTAAAGAATCTTCTGTTAGTGTCACCAGCCCCTCTGGA GTCTCCTCCTCTACATCTGGAGGAGTATCCTCTACATCCAATATGCATGGGTCACTGTTA CAAGAGAAGCACGGATTTTGCACAAGTTGCTGCAGAATGGGAATTCACCAGCTGAGGTA 2020 CAAGAAAACACCGCATTCTCCATAAGTTGCTGCAAAATGGCAACTCCCTGCAGAAGTA 2080 GCAAAGATCACAGCAGGAGCCACCGGAAAGGACGTTTTCCAGGAAACCGTGAGCTCCGCA 1140 CCTTGCACGGAAGCAACGTGAAACGAGAGCAGCTGAGCCCAAAGAAGAAGAAGAACAAT GCACTTCTTAGATACCTGCTGGACAGGGATGATCCTAGTGATGCACTCTCTAAAGAACTA AGCTCAAGTCAAGAGAAGACCCTAAAATTAAGACAGAGACAAGTGAAGAGGGATCTGGA ACTICAAGTCAGGAIAAAGAGGIIAAAAIAAAGACAGAGCCIGGAGAAGAGGIICCGGGA GACTTGGATAATCTAGATGCTATTCTTGGTGATCTGACTAGTTCTGACTTTTACAATAAT 2440 TCAATGAGTTCCAGAGCAAGCGACCTTGGGCCCAAGCAGCCTGTATTCCAGGACAGCCCA **AATATCATGATTTCTCCTCGTAATCGTGGGAGTCCAAAGATAGCCTCACATCAGTTTTCT** CCTGTTGCAGGTGTGCACTCTCCCATGGCATCTTCTGGCAATACTGGGAACCACAGCTTT 1549 TCTAGCAGCTCGCTAAGTGCTCTCCATGCCATAAGCGAAGGAGTGGGGAGTTCACTCCTG CCAAGTAAAGTAAGCAATCAGGATTCCAAGAGTCCTCTGGGCTTTTATTGCGACCAAAAT CCAGTGGAGAGTTCAATGTGTCAGTCAAATAGCAGAGATCACCTCAGTGACAAAGAAGT **AAGGAGAGCAGTGTTGAGGGGGCAGAATCAAAGGGGGTCCTTTGGAAAGCAAAGGTCAT** AAAAAATTACTGCAGTTACTTACCTGTTCTTGATGACCGGGGTCATTCCTCCTTGACC 1960 GIGICCICATCCACTICCATCGGGGTCAGCICTACGICCAACTIGCATGGCTCCATGCIT GCCAAGATTACTGCACAAGCCACTGGGAAAGAC-----ACCAGCAGTATAACTTCT TGTGGGGACGGAAATGTTGTCAAGCAGGAGCAGCTAAGTCCTAAGAAGAAGAATAAT TCCATATCCTCAAATGGTAGTCATCTGGGGACTAAGCAACAGGTGTTTCAAGGAACTAAT 2591. TCTCTGGGTTTGAAAAGTTCACAGTCTGTGCAGTCTATTCGTCCTCCATATAACCGAGCA 1429 1640 1700 2380 (1489 1909 2320 1520 1880 1789 1940 2231 1580 1760 1820 2000 2060 2120 2180 2291 2200 2411 2471 2531 유 요 ò g ò g ò 윱 ò 요 셤 g g a ò 8 셤 à 8 ò g à g 8 à 엄 õ ð ò ò õ ò ö ò

2610 2830 2781 2950 2841 3010 2901 3070 2961 3130 3190 3078 3250 3198 3370 3258 3430 3378 3541 3438 3601 3498 3661 3718 2667 2721 3021 3484 3662 ITGAAAATGGAAAACCCTACTGCTGCTGGTGCTGCGGGTGATGAGGCCTATGATGCA----GGCICTATICCCACATIGCCICTICGGICTAATAGCATACCAGGGGGGAGCAGTATIG TTGGGCATTCCTGAACTTGTCAATCAGGACAGGCATTAGAGCCCAAACAGGATGCTTTC TTCCCCATGTTACCAAAGCAACCCATGTTGGGTGGGAATCCAAGAATGATGGTTAGTCAG TCCTCAGGAGACTGGGGCTTACCAAACTCAAAGGCCGGCAGAATGGAACCTATGAATTCA CCAGGTGGGGACTGGGCTATGCAGAACTCCGCAGTCAATAGGTTGGAGCCTCCTAACGTG GGGAGCGTTGGCCGGCCAGGCCAGATTACAGTTCCGCAATGACGAGCCTGCAATGGGC GGGAATATGCCAGGACTTCTTACCAGATCTAACAGTATTCCTGGGAGCAGACCGGTGATG TCCATGGAACAAGTTTCTCATGGCACTCAAAATAGGCCTCTTCTTAGGAATTCCCTGGAT ---ATGAACCAGGGTCGTGGTGGTGCACAGAACAGACAGTTAGGAAGTTCTTTGGAC GATCTTGTTGGGCCACCTTCCAACCTGGAAGGCCAGAGTGACGAAAGAGCATTATTGGAC CTGGGAATTCCGGACTTGGTCAGGGTCAAGCTCTGGAGCCACAGGCCAGATTCTTAC CAGCCTCAAGGCTCTCCAGTCATGATCAATCAAAGCCACCATGTATGGCCAGCACTAT TCTTTTAACTCTATGATGAATCAGATGAAC --- CAGCAAGGCAATTTTCCTCTCCAAGGA **ATGCACCCACGAGCCAACATCATGAGACCCCGGAACAACACCCCCAAGCAACTTAGAATG** CAGCTTCAGCAGAGGCTGCAGGGCCAGCAGTTTTTGAATCAGAGCCGACAGGCACTTGAA GTGTCTCTGGATAGCCCTGTTTCTGTTGGCTCAAGTCCTCCAGTAAAAATATCAGTGCT ATGTCCCTAGACAGC -----AGAAGCTCCACCCTCCAGTGCGAAACGTTAACAGT GAAAATTATGGCTCAAGTATGGGTGGGCCAAACCGAAATGTGACTGTGACTCAGACTCCT GACAATITIGGCGITAIGAIGGG-----GAGIGGACCIAACAGGAGIAIGAACCAACAI AACTCCATGGGAAGACCAGGAGGAGATTATAATACTTCTTTACCCAGACCTGCACTGGGT AATCCCTATGGCCAAGCAGCATCTAACCAACTGGGTTCCTGGCCCGATGGCATGTTG CAGCTGCACACTCTTCTCAGCAACACAGATGCGACAGGCCTGGAAGAAATTGACAGAGCT CCAGCACAGGGCCTCCAATGCAAGGAGGC----TTTCATCTTCAGGGACAATCACCA GCAGGACAGGGAGCTGCTATGTCTGCTGGCGGCTTTAATAACATGCAGGGGCCAGCACCCA 2500 2560 2831 2891 2842 3011 2902 3311 3199 3259 3319 3485 3379 3542 3439 3499 2651 2711 2611 2771 2668 2722 2782 2951 3071 2962 3131 3022 3191 3079 3251 3139 3371 3431 3602 g à 셤 à g à 요 ò g ò 8 ò g ò g Š 셤 δ 요 à g õ Q δ 쉱 ç 요 ò g ò 셤 ò 셤 ò 셤 ò

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on Mar 21, 1999 this sequence version replaced gi:4375895.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                               4036 CAGCAGTACAGCCACCAGACTAAACCTGCCACGTATAACATGATGCACATGAACGGCAAC 4095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4096 GGGAATCACATGGGCCCAGATGAATATCAACTCGTTGCCTATGTCTGGAATGCCTATGGGT 4155
3559 ATGAAGGTGGACCCAATGAATCCAGGTGGAGCTGGAGTTATGAGGCCCGTGATGCAAACA 3618
                                                                                                                                                                                                                                                     3833 CAGCAGCAGCAGCAGCAGCAACAGCAACAGCAACAGCAACAGCAACAGCAACAGCAAACCCAAG 3892
                                                                                                                                                                                                                                                                                                                                                                                      3953 CCCACAATGCCACAAGCTCCTCCGCAACAGTTTCCATATCAACCAAATTATGGAATGGGA 4012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhíni; Hominidae; Homo.
1 (bases 1 to 86453)
                                                                           CCCGTCTCACAGGAGGCTTTCTCAACGCACAGATGGTGGCACAGAAGAACAGGGAACTG
                                                                                                                                                 3773 CTAAGTCATCACTTCCGACAACAGGGTGGTTGTTGATGATGCAGCAGCAGCAGCAG
                                                                                                                                                                                                                                                                                                        ----CTCAA
                                                                                                                                                                                                                                                                                                                                                            CAACAACCAGATCCAGCCTTTGGTCGAGTGTCTAGTCCTCCCAATGCAATGATGTCGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4313 CCTGATCAGAAATACTGCTGACATC 4337
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94455409
AL034418.2 GI:4455409
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                                                                                                                                                                                                                                                                                                        3739 C----
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JOURNAL
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/evidence=not_experimental
/product="dJ1049G16.1 (similar to
GLUCOSAMINE-6-SULFATASE)"
/protein_id="cA840G61.1"
/db_xref="PID:e1424046"
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/db_xref="PID:e1464046"
/db_xref="PID:e1664046"
/db_xr
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AA294950 AA332792 R14440 W71227 AA304723 AA506790 N39498
AA138508 AA120567 AA727360 C00596 AA295197 AA612659"
This sequence is the entire insert of clone 1049G16. The true left end of clone dJ237J2 is at 54555 in this sequence. This sequence has been finished according to sequence map criteria as follows attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                             This sequence was generated from part of bacterial clone contigs which sequence are 20, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20
1049G16 is from the library RPCI5 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://dopac.med.buffalo.edu/ VECTOR: pCYPAC2.
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/note="LiMB5 repeat: matches 5765, .6176 of consensus"
4004, .8719
/gene="dil049G16.1"
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    293
    note="AluSx repeat: matches 4. .296 of consensus"

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/note="FRAM repeat: matches 3. 161 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .56 of consensus"
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/note="MER3 repeat: matches 9. 209 of c 5836. 5866

/note="MER3 repeat: matches 18. 47 of cc 7598. 7639

/note="2 copies 21 mer 100% conserved"

9783. 9559

/note="12 repeat: matches 2000. 2368 of 9723. 9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
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/note="MER20 repeat: matches 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1495. .1657
/note-"12 repeat: matches 2300.
2214. .2268
/note-"MER58 repeat: matches 1.
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/note="match: GSS AQ233123"
10229. .10324
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/gene="dJ1049G16.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="20"
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                                                                                                                                                                                                                                                                                                                                                    feature key.
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Best Local Sim
Matches 1285;
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                                                                                                                                              /evidence-not_experimental
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/db_xref="g164647"
/db_xref="g16
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QQQQQTQAFSPPNVTASPSMDGLLAGPTMPQAPPQQFPYQPNYGMGQQPDPAFGRVS
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W58927 W97878"
<12013. .12427
/note="match: GSS AQ035209 clone 2329M4"
13581. .13604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="19 copies 2 mer ac 95% conserved"
15732. .15921
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/note="match: STS G42545"
16761. .17000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGACCACCIAIGGCIGGAIGCAACAGIICGGIAGGCGGCAIGAGIAIGICGCCAAACCAA 1306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1187 TICCTICAGAGABAACAGAATGGATATAGACCAAACCCAAATCCTGTTGGACAAGGGATT 1246
                                                            23; Indels 177; Gaps
                                                                                                                                                                                                                                                                                                                                      /note="AluJb repeat: matches 17. .308 of consensus" 22886. .22586 //note="AluJb repeat: matches 1. .309 of consensus" 23503. .23578
                                                                                                                                                                                                                                                        HindIII fragment"
                                                                                                                                                                                                                                                                                                                                                                                                             /note-"L2 repeat: matches 2679. .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGCAATCACCATCTTCCTACCAGAACAACAACTATGGGCTCAACATGAGTAGCCCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34941 ATGCAATCACCATCTTCCTACCAGAACAACAACTATGGGCTCAACATGAGTAGCCCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.1%; Score 1084.2; DB 10; Length 86453; 86.5%; Pred. No. 5.1e-249; Arive 0; Mismatches 23; Indels 177; Ga
                           conserved"
AVYSMVHMNGSSGHMGQMNMNPMPMSGMPMGPDQKYC"
                                                   /note-"AluSg repeat: matches 1.
                          aa 1008
              17102. .17123
/note="11 copies 2 mer
18527. .18827
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Kidwai, A.S., and Ross, C.A

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                                                                                                                                                                                             Margolis, R. L., Abraham, M. R., Gatchell, S. B., Li, S. H., Kidwai, A. S., Margolis, R. L., Abraham, M. R., Gatchell, S. B., Li, S. H., Kidwai, A. S., Breschel, T. S., Stine, O. C., Callahan, C., McInnis, M. G. and Ross, C. A. Direct Submission Submission Submitted (02-DEC-1996) Psychiatry, Johns Hopkins Univ. Sch. of Med., 600 N. Wolfe Street, Meyer 2-181, Baltimore, MD 21205, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3311 TTGGGCATTCCTGAACTTGTCAATCAGGGACAGGCATTAGAGCCCCAAACAGGATGCTTTC 3370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to Hin-2 encoded by GenBank Accession
Number U19179; polyglutamine rich"
/codon_start=1
                                                1 (bases 1 to 3487)
Margolis, R.L., Abraham, M.R., Gatchell, S.B., Li, S.H., Kidwai Barschell, T.S., Stine, O.C., Callahan, C., McInnis, M.G. and Rc cDNs with long CAG trinucleotide repeats from human brain Hum. Genet. 100 (1), 114-122 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3431 CCAGCACAGGGCCTCCAATGCAAGGAGGCTTTCATCTTCAGGGACAATCACCATCTTTT
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1166. .1201
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                          1. .3487
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="20q13.13; between D20S891 and
/dev_stage="fetus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 968.2; DB ll;
Pred. No. 2.8e-22l;
...trhes 25;
                                 Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="brain"
/note="single strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_unit-cag
781 c 775
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710. 1690
/gene="CAGH16"
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/gene="CAGH16"
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93.8%;
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GGTAGTCTAATTCTTTTCCTAAATTTTTTTTCAAATTCAGGTGTGCACTCTCCCATGGCA 34582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2089
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                                                                                                                                                                                                                                                 GATAACTCTCCCAATATGAATATTACCCAACCAAGTAAAGTAAGCAATCAGGATTCCAAG 1789
                                                                                                                                                                                                                                                                                                                                                AGCAGAGATCACCTCAGTGACAAAGAAAGTAAGGAGAGCAGTGTTGAGGGGGCAGAGAT 1909
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                                                                                                                                                  ATCAGTGAAGGTGTGGGGACTTCCCTTTTATCTACTCTGTCATCACCAGGCCCCAAATTG 1729
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                                                TCTTCTGGCAATACTGGGAACCACAGCTTTTCCAGCAGCTCTCTCAGTGCCCTGCAAGCC
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H.sapiens mRNA for transcriptional intermediary factor 2.
X97674
g1877214
X97674.1 GI:1877714
                                                                                                             1466 CCGCAGGCTGCATCCATCTATCAGTCCTCAGAAATGAAGGCTGGCCATCAGGAAATTTG
                      929 CAGAGGCTGCAGGGCCAGCAGTTTTTGAATCAGAGCCGACAGGCCACTTGAATTGAAATG
                                                            CATCACTTCCGACAACAGAGGGTGGCTATGATGATGCAGCAGCAGCAGCAA------
                                                                                                                                                                 11109 CATCACTTCCGACAACAGAGGGTGGCTATGATGATGATGAGCAGCAGCAACAGCAGCAACAG
                                                                                                                                                                                                                  CAAATTATGGAATGGGACAACAACC----AGATCCAGCCTTT-GGTCGAGTGTCT-AGT
                                                                                                                                                                                                                                                                                                                                                                                  CAAATTATGGGAATGGGGACCAACCAACAAGATCCAGCCTTTGGGTCGAGTGTCTAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                       ACCICTIAAGGAAACCACIGIACAAAIGACACIGCACIAGGAITAIIGGGAAGGAAICAI
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                                                GAAAACCCTACTGCTGGTGGTGCTGCGGTGATGAGGCCTATGATGCAGC----
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DEFINITION ACCESSION

NID VERSION

HSTIFZGEN

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/product="transcriptional intermediary factor 2"
/product="transcriptional intermediary factor 2"
/product="transcriptional intermediary factor 2"
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NRPVGGGMIRNPAASIPMRPSSQPGGRQTLQSQVMNIGPSELEMNMGGPQYSQQAPP
NGTAAWPESILLDIQASFASQNRQPFGSSPDDLLCPRHAARSPSBEGALLDOLYLALR
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SYSPMODPNFFTMGQRRSYATLRMQPRPGLRFTGLVQNQPNOLRLQLQHRLQAQQNRQ
PLANQISNVSNVNLTLRPGVPTQAPINAQMLAQRQHEILNOHLRQRQMHQQQQYQQRT
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ANTSMYSNNMNINVSMATNTGGMSSMNQMTGQISMTSVTSVPTSGLSSMGPEQVNDPA
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                                                                                                                                             Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6156)
Voegel,J., Helme,M.J., Zechel,C., Chambon,P. and Gronemeyer,H.
TIF2, a J60 kDa transcriptional mediator for the ligand-dependent activation function AF-2 of nuclear receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function="transcriptional mediator for ligand-dependent activation function AF-2 of nuclear receptors"
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    TIF2 gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (22-APR-1996) J.J. Voegel, IGBMC Inst.de Genet.et
Bholl-Mol-et-Gell, CNRS-INSERW-Univ.Louis Pasteur, B.P.163,
Strasbourg, F-67404 ILLENTRCH CEDEX, FRANCE
Revised by author 25-JUL-96 and 10-MAR-97
On Mar 11, 1997 this sequence version replaced gi:1490315.
Related sequences 139060, 403966.
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1493 c 1406 g 1458 t
    nuclear receptor coactivator;
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/db_xref="taxon:9606"
/clone_lib="lambdaEXLox Ref.No.56"
/tissue_type="placenta"
163. 4557
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2768. .2974
/gene="TIF2"
alternatively spliced; nutranscriptional mediator.
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/gene="TIF2"
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        alternatively
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AUTHORS
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JOURNAL
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Que Bes Mat	Query Match 12.4%; Score 559.4; DB 10; Length 6156; Best Local Similarity 51.0%; Pred. No. 1.5e-123; Matches 2197; Conservative 0; Mismatches 1836; Indels 276; Gaps 26:		qq	11
,			οy	11
<u> </u>	64 CAGTIGCIGAIGTAIATICAAGAIGAGIGGATTAGGAGAAAACTIGGATCCACIGGC 120 		g	12
8 8	CAGTGATTCACGAAAACGCAAATTGCCATGCGATACTCCAGGACAAGGTCTTACCTGCAG		Qy	11
음	GCCAGAGACAAGGAAGGAATGTCCTGACCAACTTGGACCCAGCCCCAAAAGGAA		q	12
ô	181 TGGTGAAAAACGGAGAGGGAGCAGGAAAGTAAATATAGAGAATTGGCTGAGCTGAT 240		δ	17
; <u>8</u>			qq	13
ò		•	δ	13
	TITIGCAAAITTIAATGATATAGACAACTITAACTICAAACCTGACAAATGTGCAATCTT		qq	14
ð	AAAGGAAACAGTAAGACACATACGTCAAATAAAAGAGCAAGGAAA AACTATTTCCAA	÷	ò	13
7 음			đ	14
٥			δ	14
음	CATAGATGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		q	15
ò	CTCCTTAGGACGCCTTTTACTTCAGGATTGGATTGGTTTTCTTATTTGTGGTATTGAGA		οy	14
급			QD	15
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3 A	*,0		qq	16
2	CCTGGTTABACACACTGTTTACABTATCTTACABGABCACACABGABACACABACABACABACABACABA		δ	15
7 A			qq	16
ò	GAATTTACCAAAATCTACAGTTAATGGAGTTTCCTGGACAAATGAGCCCCAAAAGACA	_	δλ	16
7 A	AAACCIGCIGCCAAAGICTATAGTAAATGGGGAACTCTIGGCGAACCTCCGAGGCG		q Q	17
2	AAAAAGCCATACATTTAATTGCCGTATGTTGATGAAAACACCACATGATGTTGTTGATGAAAACAC		ογ	17
			Д	18
	いまがからいことの中心の中のなりをなるのではないをはないます。		δλ	17
. d	GGGTCATGATAACCAGGAAGCTCATCAGAAATATGAAACTATGCAGTGCTTCGCTGTCTC		អូ	18
ò	775 TCAGCCACGAGCTATGGAGGAAGGGAGGAAGATTTGCAATCTTGTATGATCTGTGGC 834		ογ	18
· 8			ф	19
ò	835 ACGCCGCATTACTACGAGAAAGAACATTTCCATCAAACCCTGAGAGCTTTATTATTACCAG 894		δý	18
음	AAGAAGATICCCAIGAAGGAAAGACCAGITCITCCCTCATCAGAAGATITIACTACTCG		đ	19
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S 8	CCAGGANCTCCAAGGATCACCATGAACCACACACACACACAACAACCATGAACCATGAACAACAACAACAACAACAACAACAACAACAACAACAAC		ΩĐ	20
ò	GCCTGGCTTTGAAGATATAATCCGAAGGTGTATTCAGAGATTTTTTTAGTCTAAAGG	•	γo	19
: A	ACCAGGCTGGGAGGACCTGGTAAGAAGGTGTATTCAGAGGTTCCATGCGCAGCATGAAGG		QQ	21
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, vo	1072 AACCCCAGTATATCGATTCTCGTTGGTGGAACTATAGTGACTGCACAGACAAAAG 1131		δλ	20

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2484 TCCTGCCAGTAACACAAAATTAATAGCAATGAAAACTGAGAAGGAGGAGATGAGCTTTGA 2543 GACAAGTGAAGAGGATCTGGAGACTTGGATAATCTAGATGCTATTCTTGGTGATCTGAC 2508 2604 2664 2817 2963 3051 3111 GTCTACACATGGAACCTCGCTCAAGGAGAAGCATAAAATTTTGCACAGACTCTTGCAGGA 2249 CCAGGAGTCCAGCAGCACCACCTGGATCAGAAGTGACTATTAAACAAGAGCCGGTGAG 2369 TGATGCACTCTCTAAAGAACTACAGCCCCAAGTGGAAGGAGTGGACAATAAAATGAGTCA 2388 GIGCACCAGCTCCACCATTCCTAGCTCAAGTCAAGAGAAAAAGACCCTAAAATTAAGACAGA 2448 GCCTGGTGACCAGCCTGGAGCTGGACAACTTGGAGGAGATTTTGGATGATTTGCA 2603 2664 TGACAAGCAAGCCATCATCAATGACCTCATGCAACTCACAGCTGAAAACAGCCCTGTCAC 2723 ACCAGGGCAACTGGGCAGGTTATTGCCAAACCAGAATTTACCACTTGACATTGACATTGCA 2843 C---TGGCCCGATGGCATGTTGTCCATGGAACAAGTTTCTCATGGCACTCAAAATAGGCC 3168 TAGTICTGACTTTTACAATAATTCCATATCC-----------TCAAA 2544 2604 GAATAGTCAAITACCACAGGTTTTCCCAGACACGAGGCCAGGCGCCCCTGCTGGATCAGT 2663 CCCTGTTTCTGTTGGCTCAAGTCCTCCAGTAAAAAATATCAGTGCTTTCCCCATGTTACC 2964 CAGTAGCACAGGAATGATTGGTAACAGTGCTTCTCGGCCTACTATGCCATCTGGAGAATG 3024 GGCACCGCAGAGTTCGGCTGTGAGAGTCACCTGTGCTGCTACCACCAGTGCCATGAACCG 2904 ACCTCAGCCAGGAATGATGGTAATCAAGGGATGATAGGAAACCAAGGAAATTTAGGGAA GACTCAGACTCCTTCCTCAGGAGACTGGGGCTTACCAAACTCAAAGGCCGGCAGAATGGA 3084 GCCAGICCAAGGAGGIAIGAIICGGAACCCAGCAGCAGCACCAICAGCAGCCCAAGCAG CCAGCCTGGCCAAAGACAGACGCTTCAGTCTCAGGTCATGAATATAGGGCCATCTGAATT CCCCATGGGAATGGGGGCTAATCCCTATGGCCAAGCAGCAGCATCTAACCAACTGGGTTC AGAGATGAACATGGGGGGACCTCAGTATAGCCAACAACAAGCTCCTCCAAATCAGACTGC TCCTAAGAAGAAGGAGAATAATGCACTTCTTAGATACCTGCTGGACAGGGATGATCCTAG **TGGTAGTCATCTGGGGACTAAGCAACAGGTGTTTCAAGGAACTAATTCTCTGGGTTTGAA** AAGTICACAGICIGIGCAGICIAIICGICCICCAIAIAAACCGAGCAGIGICICIGGAIAG ACCTGTTGGAGCCCAGAAAACAGCACTGCGAATTTCACAGAGCACTTTTAATAACCCACG 2844 AAGCCCAACTGGTGCTGGACCTTTCCCAACTCAGAAACAGTAGTCCCTACTCAGTGAT 2878 ACCTATGAATTCAAACTCCATGGGAAGACCAGGAGGAGATTATAATACTTCTTTACCCAG ----GCGAGACCAGTATTGCAACAGCAGCAGATGCTTCAAATGAGGCCTGGTGAAAT ------CAGTATAACTICTTGTGGGGACGGAAATGTTGTCAAGCAGGAGCAGCTAAG ACCIGCACIGGGIGGCICIATICCCACATIGCCICITCGGICIAAIAGCAIACCAGGI - -TGGGAATTCACCAGCTGAGGTAGCCAAGATTACTGCACAAGCCACTGGGAAAGACACCAG AAAGCAACCCATGTTGGGTGGGAATCCAAGAATGATGGATAGTCAGGAAAATT-----2158 2218 2310 2269 2370 2329 2389 (2725 2778 2938 3144 3052 3112 2190 2427 2545 2724 2665 2784 2818 2996 2449 2544 2509 2605 S S 윱 유 ö ď ö 셤 ò a ò g õ 요 ò 셤 9 6 oy B ò 8 õ 셤 3 à 임 ò g ò g ò 원 ò

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KARDISSSSSPAQALCSGNPGODMTLGSNINRPMGPREQMSHWGHREGGSGGMNHV
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PAGSLHSPVGVCSSTGNSHSYTNSSLNALQALSEGHGVSLGSSLASPDLKMGNLONSP
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SSTGGGVIDKDALGPMALEALDGFFFVVNLEGSSVVFVSENVTQYLRYNQEELMNKSVY
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                                     MMU39060 4878 bp mRNA ROD 25-APR-1997
Mus musculus glucocorticoid receptor interacting protein 1 (GRIP1)
                                                                                                                                                                                                                                                                                                                                                                                                     Hong, H., Kohli, K., Garabedian, M.J. and Stallcup, M.R.
Scribt, a transcriptional coactivator for the AF-2 transactivation
domain of steroid, thyroid, retinoid, and vitamin D receptors
Mol. Cell. Biol. 17 (5), 2735-2744 (1997)
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1167 to 3560) Hong, H., Kohli, K., Trivedi, A., Johnson, D. L. and Stallcup, M.R. GRIPI, a novel mouse protein that serves as a transcriptional coactivator in yeast for the hormone binding domains of steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="glicocorticoid receptor interacting protein
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/db_xref="PID:g1853980"
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Submitted (20-OCT-1995) Department of Pathology, University of
Southern California, 2011 Zonal Ave. HMR 301, Los Angeles, CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence and feature updates by submitter
On Feb 28, 1997 this sequence version replaced gi:1314284
Location/Qualifiers
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Hong, H. and Stallcup, M.R.
Direct Submission
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180 240 361 300 417 541 601 64 CAGTIGCTGATGTATATICAAGATGAGTGGATTAGGAGAAAACTTGGATCCACTGGCCAG 123 301 421 357 481 418 CICCTIAGGACCGCTITIACTICAGGCAITGGAIGGIITCCIATITGIGGIGAAICGAGA 477 537 661 597 721 Gaps GAA----TITACCAAAATCTACAGTTAATGGAGTTTCCTGGACAAATGAGCCCCCAAAGACA 654 302 CACTGAGAAACGGAAACCGCGAGCAGGAGAATAAGTACATAGAGGAGCTGGCCGATCTGAT 538 CCTGGTTAACACAAGTGTTTACAATATCTTACATGAAGAAGACAGAAAGGATTTTCTTAA 662 GCTGATGAACAAGAGTGTCTACAGCATCCTGCATGTCGGGGACCACACAGAATTGTCAA 182 CAGTIGCIGATATGTGTTCAAGATGAGTGGGATGGGAGAAAACACCTCTGACCCGTCCAG 124 T---GATTCACGAAAACGCAAATTGCCATGTGATACTCCAGGACAAGGTCTTACCTGCAG 242 GGCAGAGACCAGAAAACGCAAGGAATGTCCCGACCAGCTCGGACCCAGCCCCAAAAGGAG 478 GGCAAACATTGTATTGTATCAGAAAATGTCACACAATACCTGCAATATAAGCAAGAGGA 181 TGGTGAAAAACGGAGAGCGGAGCAGCAAAGTAAATATATTGAAGAATTGGCTGAGCTGAT 241 ATCTGCCAATCTTAGTGATATTGACAATTTCAATGTCAAACCAGATAAATGTGCGATTTT 301 AAAGGAAACAGTAAGACAGATACGTCAAATAAAAGAGCAAGGAAA---AACTATTTCCAA 358 TGATGATGATCAAAAAGCCGATGTATCTTCTACAGGGCAGGGAGTTATTGATAAAGA Query Match 11.5%; Score 517; DB 12; Length 4878; Best Local Similarity 51.1%; Pred. No. 2e-113; Matches 2204; Conservative 0; Mismatches 1815; Indels 298;

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, d	1245	TTAGACCACCTATGGCTGGATGCAACAGTTCGGTAGGCGGCATGAGTATGTCGCC 1299	
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S q	1360	AGGCAGATGAGTGGAGCTAGGTATGGGGGTTCCAGTAACATAGCTTCATTGACCCCTGG 1419	
6 8	1420 1553	GCCAGGCATGCAATCACCATCTTCCTACCAGAACAACAACTATGGGC	
	1480	CCCCCCACATGGGAGTCCTGGTCTTGCCCCAAACCAGCAGAATATCATGATTTCTCCTCG 1539	
ر م	1540	TAATGG	
6 6y	1582	TGTTGCAGGTGTGCCATGCCATGGCATCTTCTGGCAATACTGGGAACCACAGCTT 1638 	
S G	1639 1790	TICCAGCAGCTCTCTCAGIGCCCTGCAAGCCATCAGTGAAGGTGTGGGGACTTCCCTTTT 1698 	
č q	1699	ATCTACTCTGTCATCACCAGGCCCCAAATTGGATAACTCTCCCAATAT 1746 	
g ç	1747	GAATATTACCCAACCAAGTAAAGTAAGGAATCAGGATTCCAAGAGTCCTCTGGGCTTTTA 1806 	
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2878 2823 2871 2089 1971 2031 2197 2091 2151 2211 2344 2262 2322 2461 2382 2521 2442 2578 2502 2638 2544 2598 2758 2658 2773 1970 TGGGGAGCCCTCAGAAGGTACAACTGGACAAGCAGAGGCCAGCTGCCATCCTGAAGAACA 2029 2224 2284 CGTCCCACCTGCCGGAGCCCAGAAGGCAGCACTGCGCATGTCACAGAGCACTTTTAATAA 2818 GCTGAGCCAGGAGTCCAGCAGCACACCTCCTGGGTCGGAAGTGACTGTCAAACAGGAGCC 2404 2405 AGCGAGCCCCAAGAAGAAGAG---AATGCACTACTGCGCTATTTGCTCGACAAGATGA TICTGTIAGTGTCACCAGCCCCTCTGGAGTCTCCTCCTCTACATCTGGAGGAGTATCCTC 2092 TACATCCAATATGCATGGGTCACTGTTACAAGAGGAGCACCGGATTTTGCACAAGTTGCT 2462 TACTAAAGATATTGGTTTACCGGAAATAACCCCCAAACTCGAGCGACTGGACAGTAAGAC 2522 AGAICCIGCCAGIAACACAAAGIIAAIIGCIAIGAAAACIGIGAAGGAG---GAGGIGAG 2819 CCCACGACCAGGGCAACTGGGCAGGTTATTGCCAAACCAGAACTTACCACTTGACATCAC 2879 TITGCAAAGCCCAACTGGTGCTGGACCTTTCCCACCAATCAGAAACAGTAGCCCCTACTC 2823 --AGACTCCTTCCTCAGGAGACTGGGGCTTACCAAACTCAAAGGCCGGCA------TGATGACCGGGGTCATTCCTCCTTGACCAACTCCCCCCTAGATTCAAGTTGTAAAGAATC GCCTGGGTCCACGCATGGCACCTCGCTCAAGGAGAAGCATAAAGATTTTGCACAGACTCTT 2152 GCAGAATGGGAATTCACCAGCTGAGGTAGCCAAGATTACTGCACAAGCCACTGGGAAAGA 2285 ACAGGACAGCAGTTCCCCTGTGGACTTGGCCAAGCTGACAGCAGAAGCCACAGGCAAAGA 2212 CACCAG------CAGTATAACTTCTTGTGGGGACGGAAATGTTGTCAAGCAGGAGCA TCCTAGTGATGCACTCTCTAAAGAACTACAGCCCCAAGTGGAAGGAGTGGACAATAAAAT 2383 GAGTCAGTGCACCAGCTCCACCATTCCTAGCTCAAGTCAAGAGAAAAAGACCCTAAAATTAA 2443 GACAGAGACAAGTGAAGAGGGATCTGGAGACTTGGATAATCTAGATGCTATTCTTGGTGA 2579 CTTTGAGCCCAGTGACCAGCCTGGAGCTGGACAACTTGGAAGAGTTTTGGATGA TITGCAGAACAGICAGITACCACAGCITITCCCAGACACAAGGCCAGGAGCTCCTACTGG ----ATGGTAGTCATCTGGGGACTAAGCAACAGGTGTTTCAAGGAACTAATTCTCTGGG GTCAGTTGACAAGCCATCATCAATGACCTCATGCAACTCACAGCTGACAGCAGTCC TITGAAAAGTICACAGICIGIGCAGICIAIICGICCICCAIAIAACCGAGCAGIGICICI GGATAGCCCTGTTTCTGTTGGCTCAAGTCCTCCAGTAAAAAATATCAGTGCTTTCCCCAT GTTACCAAAGCAACCCATGTTGGGTGGGAATCCAAGAATGATGGATAGT-----CAGGAA -AGAGATCACCTCAGTGACAAAGAAAGTAAGGAGAGCAGTGTTGAGGGGGCAGAGAATCA ------ACAAGGACTTGAACAGGAGCTTGCCTGG GCTAAGTCCTAAGAAGAAGGAGAATAATGCACTTCTTAGATACCTGCTGGACAGGGATGA AATTATGGCTCAAGTATGGGTGGGCCAAACCGAAATGTGACTGTGACTC------1972 2150 2032 2345 2503 2639 2544 2699 2599 2759 2659 2774 1853 1912 2225 2263 2323 2939 2197 2719 g g 셤 δ 요 å g ò ద ò g ò ద ő 2 2 2 å g à g ŏ ద õ ò 셤 ò à ద ò ద ò 셤 ò g

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              3059 GGAATGGGCACCACAGAGTCCAGCT--GTGAGAGTCACTTGTGCTGCTACCACTGGTGCC
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                                                                              GCATACCAGGTGCGAGACC - AGTATTGCAACAGCAGCAGCAGATGCTTCAAATGAGGCCT
                                                                                                                                  GCCAACAGCCAGCCTGGCCAAGACAGATGCTTCAGTCTCAGGTCATGAACATAGGCCCT
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EAHORYETMOCFAVSOPKSIREEGEDKQSCLICVARRYPWKERPALPSSESFTTRODL
GGKITFLDJSTMRDAMKPGWEDLVRRCIQKFHTQHEGESLSYAKRHHEVLROGLAFS
QIYRFSLSDGTLVAAQTKSKLIRSQTTNEPQLVISIHMLHREQNVCVMNPDLTGQAMG
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/translation="MGGMGENYSDPSRAETRRRRECPDOLGPSPRRSTERRNREDENK
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SSTGQGVIDROALGPMALEALOGFFFVYNLEGNYVFVSENYTQYLRYNOBELMNRSYY
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SGMQATTPQGSNYALKMNSPSQSSPGLNPGQPSSVLSPRHRMSPGVAGSPRVPPSQFS
PAGSLHSPAGVCSSTGNSHSYTNSSLNALQALSEGHGVSLGPSLASPDLKMGNSQNSP
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LKEKHKILHRLLQDSSSPVDLAKLTARATGKELNOESSGTAPGSEVTVKQEPASPKKK
ENALLRYLLDKDDTKDIGLPEITPKLERLDSKTDPASNTKLIAMKTVKEEVSFEPSDQ
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3941 CTTTTGGCAGGACCCACAATGCCACAAGCTCCTCCGCAACAGTTTCCATATCAACCAAAT 4000
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Leers,J., Treuter,E. and Gustafsson,J.-A.
Mechanistic principles in NR box-dependent interaction between nuclear hormone receptors and the coactivator IFF2
Mol. Cell. Biol. 18 (10), 6001-6013 (1998)
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Rattus norvegicus transcriptional intermediary factor 2 (TIF2)
MRNA, complete cds.
ARI36943
94581052
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Direct Submission
Submitted (24-MAR-1999) Department of Biosciences, Karolinska
Institute, Haelsovaegen 7, Huddinge 14157, Sweden
                                                                                                                                                                                                                                                                                                                                                                4178 AGCICCTITICCCAGCAGCAGTITGCCCACCAGGGGAATCCIGCAGIGIATAGTAIG 4234
                                                                                                                                                                                                                                                                                                                                                                                                             AGCATGTTCTCACAGCAGTCCCCACCACCACTTTGGGCAACAACAACACCAGCATG 4346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="nuclear hormone receptor coactivator"
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/db_xref="PID:94581053"
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31; 480 262 300 360 499 420 559 142 202 9 ATGAGTGGATTAGGAGAAAACTTGGATCCACTGGCCAG---TGATTCACGAAAACGCAAA ATGAGTGGGATGGGAGAAAATACCTCTGACCCGTCCAGGGCAGAGACCCAGAAACGCAAG GAATGTCCGGACCAGCTCGGACCCCAAAAGGAGCACGGAGAAACGTAACCGCGAG TTGCCATGTGATACTCCAGGACAAGGTCTTACCTGCAGTGGTGAAAAACGGAGACGGGAG CAGGAAAGTAAATATATTGAAGAATTGGCTGAGCTGATATCTGCCAATCTTAGTGATATT GACAATTTCAATGTCAAACCAGATAAATGTGCGATTTTAAAGGAAACAGTAAGACAGATA CGTCAAATAAAAGACAAGGAAAAACT---ATTTCCAATGATGATGATGTTCAAAAAGCC GATGTATCTTCTACAGGGCAGGGAGTTATTGATAAAGACTCCTTAGGACGGCTTTTACTT CAGGCATTGGATGGTTTCCTATTTGTGGTGAATCGAGAGGCAAACATTGTATTTGTATCA GAGGCCCTTGATGGTTTTTTTTTCGTCGTGAACCTAGAAGGCAATGTGGTGTTCGTGTCC GAGAACGTGACGTATTCTCCGGTATAACCAGGAAGAACTGATGAACAAGAGCGTTTAC GAAAATGTCACACAATACCTGCAATATAAGCAAGAGGACCTGGTTAACACAAGTGTTTAC Indels Score 499.8; DB 12; Pred. No. 2.6e-109;); Mismatches 1802; LRGSSLFTINQLPGMDMIKQEGDGSRKYC" 1232 c 1125 g 808 t ,, 11.1%; ilarity 51.0%; Conservative Query Match Best Local Similarity Matches 2195; Conserv 1233 BASE COUNT ORIGIN 98 143 121 181 241 440 61 203 263 323 380 301 361 200 421 8 g g g g ð ò ô g ò g ò 6 S ð

1260 1441 1371 1548 1660 1608 1720 1668 1768 1933 1093 1020 1153 1261 1200 1321 1381 1320 1501 1428 1603 CGAAGGTGTATTCAGAGATTTTTAGTCTAAATGATGGGCAGTC---ATGGTCCCAGAAA 1549 GCGGGAGTTTGCAGCACACAGGAAATAGCCATAGTTACACCAACAGTTCCCTCAATGCA -----AGGAGAGCAGTGTTGAGGGGCCAGAGAATCAAAGGGGTCCTTTGGAAAGCAAA 917 GTCAATATAGATACAAATTCACTGAGATCCTCCATGAGGCCTGGCTTTGAAGATATAATC CGTCACTATCAAGAAGCTTATCTTAATGGCCATGCAGAAACCCCCAGTATATCGATTCTCG TTGGCTGATGGAACTATAGTGACTGCACAGACAAAAAGCAAACTCTTCCGAAATCCTGTA 1201 AGCAGCCCGCCCGTCAGGCCATGTGCAGTGGGAACCCAGGTCAGGACGTGGCCCTCGGT AGCAATATGAACTTTCCCATGAATGGCCCAAGGGAACAGATGAGCATGCCTATGGGCAGG CC---TCAGGGTAGTAACTATGCACTCAAAATGAACAGTCCCTCACAAAGCAGCCCCGGC 1489 GCTGGCAGTCCTCGCGTTCCACCCAGTCTTTCCCCTGCAGGAAGCTTGCACTCCCCA ATGGCATCTTCTGGCAATACTGGGAA - - - CCACAGCTTTTTCCAGCAGCTCTCTCAGTGCC CCCAAATTGGATAACTCTCCCAAT------ATGAATATTACCCAACCAAGTAAA GTAAGCAATCAGGATTCCAAGAGTCCTCTGGGCTTTTATTGCGACCAAAATCCAGTGGAG ATGGGAAGCTTGGACTCCAAAGACTGTTTTGGACTTTATGGGGAGCCATCAGAAGGTACA AGTTCAATGTGTCAGTCAAATAGCAG-----AGATCACCTCAGTGACAAAGAAAGTA--901 AGAAGATCTATTCAGAAGTTCCACACACCATGAAGGGGAGTCTCTATCATACGCCAAG 1141 GTAATGAATCCGGATCTGACTGGACAAGCAATGGGGAAGCCATTGAGTCCAATGAGCTCT GGATGCAACAGTTCGGTAGGCGGCATGAGTATGTCGCCAAACCAAGGCTTACAGATGCCG 1442 TCCTACCAGAACAACAACTATGGGCTCAACATGAGTAGCCCCCCCACATGGGAGTCCTGGT CTTGCCCCAAACCAGCAGAATATCATGATTTCTCCTCGTAATCG---------CIGAACCCAGGCAACCCAGCICIGIGCICICCCCACGGCAICGCAIGAGCCCCGGCGIG -- TGGGAGTCCAAAGATAGCCTCACATCAGTTTTCTCCTGTTGCAGGTGTGCACTCTCCC CTGCAAGCCATCAGTGAAGGTGTGGGGACTTCCCTTTTATCTACTCTGTCATCACCAGGC TTGTCAGACGGCACTCTCGTTGCTGCACAAACGAAGAGAAAACTCATCGTTCCCAGACT AGACCAAACCCAAATCCTGTTGGACAAGGGATT-------AGACCACCTATGGCT **AGCAGCAGGGCCTATGGCTTGGCAGACCCTAGCACCACAGGGCAGATGAGTGGGCTAGG** TATGGGGGTTCCAGTAACATAGCTTCATTGACCCCTGGGCCAGGCATGCAATCACCATCT 1729 1081 1604 1609 1721 1769 1789 1034 961 1094 1021 1154 1214 1322 1261 1382 1372 1502 1429 1546 1669 1829 1881 977 1262 1661 g 셤 g g õ g ò ద ò ద ò g ö 셤 δy g ŏ g ò 8 à ò ద à g ö 셤 à 셤 원 å 8 ò à ò ò

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2113 2223 2811 TGACTGTGACTCAGACTCCTTCCTCAGGAGCTGGGGGCTTACCAAAGTCAAAGGCCGGCA 2870 1849 ATGCCCCAGGCGCCAGCGAGGACAGGGCTGAGGGACACAGCCGGCTGCATGAGAGCAAA 1908 AATAATGCACTICTTAGATACCTGCTGGACAGGGATGATCTAGTGATGCCACTCTCTAAA 2344 GAACTACAGCCCCAAGTGGAAGGAGTGGACAATAAAATGAGTCAGTGCACCAGCTCCACC 2404 2281 GAAATAACCCCCAAACTCGAGCGGTTGGACAGTAA---GACAGATCCTGCCAGTAACACA 2337 2398 GGCAGCGAGCTGGACAACTTGGAAGAGTTTTGGATGATTTGCAGAATAGTCAGTTACCA 2457 AAGGAACTAATTCTCTGGGTTTGAAAAGTTCACAGTCTGTGCAGTCTATTCGTCCTCCAT 2639 AAAGCAGCACTGCGAATGTCACAGAGCACTTTTAATAACCCACGACCAGGGCAACTGGGC 2637 2816 TGATTGGCAGTAGCACTTCCCGGTCCAGCATGCCTTCTGGGGGAATGGGCACCACAGAGTC 2875 2876 CAGCTGTGAGAGTCACTTGTGCTGCCACCACTGGTGCCATGAACCGGCCAATCCAAGGGG 2935 GAGGTAGCCAAGATTACTGCACAAGCCACTGGGAAAGACACCA------GCAGTATA 2224 2338 AAGCTAATCGCCATGAAAACTGTGAAGGAGGAGGTGAGCTTTGAGCCCAGTGACCAGCCT 2397 -----TGGGAAGACCAGGAGGAGATTATAATACTTCTTTACCCAGACCTGCACTGGGTG 2951 GGTCATAAAAATTACTGCAGTTACTTACCTGTTCTTGATGACCGGGGTCATTCCTCC 1909 GGGCAAACCAAACTCCTACAGCTGCTCACCAAGTCCGACCAGATGGAGCCTTCACCC 1969 TTGCCCAGCTCTTTGTCGACACAA------TCTGGAGTCTCCTCCTCTACATCTGGAGGAGTATCCTCTACATCCAATATGCATGGGTCA -----ACAAGGACTCCACAGGCAGCTTGCCAGGGCCTGGGTCCACGCATGGCACC CTGTTACAAGAAGCACCGGATTTTGCACAAGTTGCTGCAGAATGGGAATTCACCAGCT **ACTICITGIGGGACGGAAATGITGTCAAGCAGGAGCAGCTAAGTCCTAAGAAGAAG** 2224 AAC---GCACTACTGCGCGTATTTGCTCGACAAGATGATACTAAAGATATTGGTTTACCG 2405 ATTCCTAGCTCAAGTCAAGAGAAAAGACCCTAAAATTAAGACAGAGAAAGTGAAGAGGGGA 2465 TCTGGAGACTTGGATAATCTAGATGCTATTCTTGGTGATCTGACTAGTTCTGACTTTTAC AATAATTCCATATCCTCAAATGGTAGTCATC----TGGGGACTAAGCAACAGGTGTTTC ATCAATGACCTCATGCAACTCACGGCTGACAGCAGTCCTGTCACACCTGTCGGAGCCCAA 2640 ATAACCGAGCAGTGTCTCTGGATAGCCCTGTT------CTGTTGGCTCAAGTCCTC TTGACCAACTCCCCCCTAGATTCAAGTTGTAAAGAATCTTCTGTTAGTGTCACCAGCCCC 2638 AGGTTATTGCCAAACCAGAATTTACCACTTGACATCACATTGCAAAGCCCAACTGGTGCT 2871 GAATGGAACCTATGAATTCAAACTCCA------2054 2114 2174 2164 2580 2578 1934 1994 1994 2225 2285 2525 2518 용 g g 셤 g g ద g g a 음 õ g ò g g g 8 ò ò ò ò ò ö ò ò ç ò ö ð ö å

3122 3302 3289 3362 3349 3422 3403 3482 3463 3542 3596 3656 3616 3716 3673 3808 4016 GAGGCCCTCAGTATAATCAACAGCAGCCCCTCCAAACCAAACTGCCCCTGGCCCGAGA 3115 3674 CAACT---CAGGCTCCTATCAATGCACAGATGCTGGCCCAGAGGCAGAGGGAAATCCTTA 3730 3869 GGATCCCGCAAGCCAATGCCCAGTTTCCATTCCTCCGAACTACGGAATAAGTCAGC 3928 GCTCTATT-----CCCACATTGCCTCTTCGGTCTAATAGCATACCAGGTGCGAGACCAG 3005 3236 TICTAGACCAGCTCTATCTGGCCTTGCGGAACTTCGAT-----GGCCTTGAAGAGATTG GGGCTAATCCCTATGGCCAA---GCAGCAGCATCTAACCAACTGGGTTCCTGGCCCGATG AGCCCCAGCAGGGTTTCTTAATGCTCAAATGGTCGCCCAACGCAGCAGAGAGCTGCTAA -------ACCAGCATCTCCGGCAGA GCAIGIIGICCAIGGAACAAGIIICICAIGGCACICAAAAIAGGCCICIICIIAGGAAII CCCTGGATGATCTTGTTGGGCCACCTTCCAACCTGGAAGGCCAGAGTGACGAAAGAGCAT ACAGAGCTTTGGGCATTCCTGAACTTGTCAATCAGGGACAGGCATTAGAGCCCAAACAGG AGACATACCCAGCACAGGGGCCTCCAATGCAAGGAGGCTTTCATCTTCAGGGACAATCAC CATCTTTTAACTCTATGATGAATCAGATGAACCAGCAAGGCAATTTTCCTCCAAGGAA TGCACCCACGAGCCAACATCATGAGACCCCGGACA-----AACACCCCCAAGCAACTTA TGCAGCCCCGGCCCTCAGGCCCACAGGCATTGTGCAGAACCAGCCAACCTGA GAATGCAGCTTCAGCAGAGGCTGCAGGGCCAGCATTTTGAATCAGAGCCGACAGGCAC GACTTCAGCTCCAACATCGCCTCCAAGCACAG-------CAGAACCGCCAGCCGC TTGAATTGAAAATGGAAAACCCTACTGCTGGTGGTGCTGCGGTGATGAGGCCTATGATGC T---AATGAACCAGATCAGCGGCGTTTCCAATGTGAACTTGACTTTGAGGCCTGGCGTGC TGAATATGACCCCAAGCATGGTGGCTCCCACTGGTTTACCAGCAGCCATGAGCAACCCCC CAATGCCACAAGGTCCTCCGCAACAGTTTCCATATCAACCAAATTATGGAATGGGACAAC TATTGCAACAGCAGCAGCAGATGCTTCAAATGAGGCCTGGTGAAATCCCCCATGGGAATGG TATTGGACCAGCTGCACACTCTTCTCAGCAACACAGGATGCGACAGGCCTGGAAGAAATTG 3363 ATGCTTTCCAAGGCCAAGAAGCAGCAGTAATGATGATGGATCAGAAGGCAGGATTATATGGAC GTCATCACTTCCGACAACAGGGTGGCTATGATGATGCAGCAGCAGCAGCAGCAGCAGC 3837 AGCAGCAGCAGCAGCAGCAACAGCAACAGCAGCAGCAACAGCAACCCAGGCCT 3483 3957 2936 3006 2996 3116 3176 3243 3303 3290 3349 3423 3404 3543 3509 3617 3777 3731 3897 3809 2952 3066 3056 3123 3183 3463 3597 3569 3657 3717 셤 셤 셤 셤 셤 δ ద g q ò g ò g g ద q 셤 셤 ò 셤 ö à ò à δ à ò ò g ò ò à ò ò ò

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STOGOVIDRALGPMALEALDGFFVVNLEGSVVFVFRNYDOYLKYNDEELMKSVY
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BAHQKYEAMQCFAVSQPKSIKREGSEDLGSCLIVWHEDPHEGKTNSSLIRKLYHPPGPP
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Submitted (21-ARR-1997) Medicine, Howard Hughes Medical Institute
at the University of California, San Diego, 9500 Gilman Drive,
the University of California, San Diego, 9500 Gilman Drive,
C.M.M. 345, La Jolla, CA 92093-0648, USA
      4076
                                                                                                                                                     3989 IGGCACATACGCAGAGTCCCATGATGCAGCAGCCTACCAGCCCG 4048
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria: Rodentia; Solurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 47).
Torchia, 7., Rose, D.W., Inostroza, J., Kamei, Y., Westin, S.,
Glass, C.K. and Rosenfeld, M.G.
The transcriptional co-activator p/CIP binds CBP and mediates
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Mus musculus nuclear receptor coactivator protein 2 mRNA, com
   AACCAGATCCAGCCTTTGGTCGAGTGTCTAGTCCTCCCAATGCAATGATGTCGTCAAGAA
                                                                                                                                                                                                                                          CCTCAGAAATGAAGGGCTGGCCATCAGGAAATTTGGCCAGGAACAGCTCCTTTTCCCAGC
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                                                                                                                      TGGGTCCCTCCCAGAATCCCATGATGCAACACCCGCAGGC---TGCATCCATCTATCAGT
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/note="NCoA-2; nuclear receptor coactivator"
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Nature 387 (6634), 677-684 (1997)
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GGXNPWQDPRTHTMGQRPNYTTLRAGPRPGLRFGIVONOPYGLKLOLOHRLOAOUN
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                                                                                                                                                                                Score 474; DB 12;
Pred. No. 3.8e-103;
0; Mismatches 1845;
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2236 AG------CAGTATAACTTCTTGTGGGGACGAAATGTTGTCAAGCAGCAGCTA 2266 2356 2506 2549 2591 CAGAACAGTCAGTTACCACAGCTTTTCCCAGACACAAGGCCAGGAGCTCCTACTGGGTCA 2650 GACCGGGGTCATTCCTCCTTGACCAACTCCCCCTAGATTCAAGTTGTAAAGAATCTTCT 2035 2156 AATGGGAATTCACCAGCTGAGGTAGCCAAGATTACTGCACAAGCCACTGGGAAAGACACC 2357 AGCCCCAAGAAGAAGAAG---AATGCACTACTGCGCTATTGCTCGACAAAGATGATACT CGAGCAGTGTCTCTGGATAGCCCTGTTTCT-----GTTGGCTCAAGTCCTCCAGTAA 2891 ATACCTCAGCCAGGAATGATGGTAACCAAGGGATGCTAGGAAGCCAAGGAAACTTAGGG CAGATGGAGCCTTCACCCTTGCCGAACAAACAAGGAC------GTTAGTGTCACCAGCCCCTCTGGAGTCTCCTCCTCTACATCTGGAGGAGTATCCTCTACA -------TCGACAGGGAGCTTGCCTGGGCCT 2096 TCCAATATGCATGGGTCACTGTTACAAGAAGCACCGGATTTTGCACAAGTTGCTGCAG 2177 GGGTCCACGCATGGCACCTCGCTCAAGGAGAAGCATAAGATTTTGCACAGACTCTTACAG AGCCAGGAGTCCAGCAGCACCAGGTCGGAAGTGACTGTCAAACAGGAGCCAGCG 2414 AAAGATATTGGTTTACCGGAAATAACCCCCAAACTCGAGCGACTGGACAGTAAGACAGAT CCTGCCAGTAACACAAAGTTAATTGCTATGAAAACTGTGAAGGA---GGAGGTGAGCTTT 2531 GAGCCCAGTGACCAGCCTGGCAGCTGGACAACTTGGAAGAGATTTTGGATGATTTG --------ACTAGITCIGACITITACAATAATICCATATCCTCAAATGGIA ----TTCTCTGGGTTTGAAAAGTTCACAGTCTGTGCAGTCTATTCGTCCTCCATATAAC 2831 CAAAGCCCAACTGGTGCTGGACCTTTCCCAACAACAGAAACAGTAGCCCCTACTCAGTG TGACTCAGACTCCTTCCTCAGGAGACTGGGGCTTACCAAACTCAAAGGCCGGC---AGAA TGGGCACCACAGAGTACCAGCTGTGAGAGTACACTTGTGCTGCTACCACTGGTGCCAAGA AGTCCTAAGAAGAAGAATAATGCACTTCTTAGATACCTGCTGGACAGGGATGATCCT **AGTGATGCACTCTCTAAAGAACTACAGCCCCAAGTGGAAGGAGTGGACAATAAAATGAGT** 2447 GAGACAAGTGAAGAGGGATCTGGAGACTTGGATAATCTAGATGCTATTCTTGGTGATCTG 2771 GACCAGGCAACTGGGCAGGTAATTGCCATACCAGAACTTACCACTTGACATCACTTTG TGGAACCTATGAATTCAAACTCCATGGGAAGACCAGGAGGAGATTATAATACTTTTAC CCAGACCTGCACTGGGTGGCTCTATT -----CCCACATTGCCTCTTCGGTCTAATAGCA GTCATCTGGGGACTAAGCAACAGGTGTTTCAAGGAACTAA-----2297 2102 2036 2216 2267 2327 2387 2474 2507 2550 2651 2590 2645 2697 2757 2817 2874 3011 2934 2153 8 g à g ò 엄 ò g à g à g à 셤 ŏ 유 ŏ ద ò g à g à g ò 셤 8 8 à 8 유 ò g ð

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2988 TACCAGGIGCGAGACC-AGTATIGCAACAGCAGCAGCAGAIGCTICAAATGAGGCCIGGT
                                       3131 AACAGCCAGCTIGGCCAAAGACAGATGCTICAGICTCAGGTCATGAACATAGGCCCTICT
                                                                                  GAAATCCCCATGGGAATGGGGGCTAATCCCTATGGCCAA---GCAGCAGCATCTAACCAA
                                                                                                                                                                    3104 CTGGGTTCCTGGCCCGATGGTTGTTCTCATGGAACAAGTTTCTCATGGCACTCAAAAT
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EVMQCFTVGOFKSTOEDGEDFQSCITCIARRLPRPAITGYESFMTKODTTGKIISID
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ITERHKILHRLLOEGSPSDITTLSVEPDKKDSASSTSVSTGQVQGNSSIKLELDASKK
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IKLEAGOSGYTADLDOPPOLLPPLEKRAAQLPGLEFETBNUGGATSVATKSEILPASLOS
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 4664)
Kalkhoven,E.
                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-1998
                                                                            4124 ATCTATCAG---TCCTCAGAATGAAGGGCTGGCCATCAGGAAATTTGGCCAGGAACAGC
                                                                                                           HSJ000881 4664 bp mRNA PRI 02-M
Homo sapiens mRNA for steroid receptor coactivator la.
AJ000881
                                                                                                                                                                                                                               4244 AIGITCICACAGCAGICCCCACACATITGGGCAACAAGCAAACACCAGCAIG
                                                                                                                                                                                     4181 TCCTTTTCCCAGCAGCAGTTTGCCCACCAGGGAATCCTGCAGTGTATAGTATG
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/cell_type="normal B cell"
/map="2p23"
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92924310
AJ000882.1 GI:2924310
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Kalkhoven, E.
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MAGGNTNVQNMNPMMAQMQMSSLQMPGMNTVCPEQINDPALRHTGLYCNQLSSTDLLK
TEADCTQQVQQVQFADVQCTVNLVGGDPYLNQPGPLGTQKPTSGPQTPQAQQKSLLQ
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                                                                                                                                                                                                                                                                                                                      216 ATATTGAAGAATTGGCTGAGCTGATATCTGCCAATCTTAGTGATATTGACAATTTCAATG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                        386 TAAAACCAGACAAATGCAAGATTTTGAAGAAACAGTCGATCAGATACAGCTAATGAAGA 445
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                                                                                                                                                             DB 10; Length 4664;
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                                                                                                                                                         Score 328.4; DB 10;
Pred. No. 2.4e-68;
0; Mismatches 406;
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Best Local Similarity 59.7'
Matches 633; Conservative
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GTMLSAHTKCKLCYPQSPDMQPFIWITHIDRRHSGLSPDDDYNSGWSTFRVNPSVNP
SITSPAHGVARSSTLPSPSNSWMYSTRINGQSSDLASSSHSNSSNSQGSFGGSGGLY
ANVALNQGGASSQSSNPSLNLNNSPMEGTGISLAQFMSPRRQYTSGLATRPRMPNNSF
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EVMQCFTVSQPKSIQEDGEDFGSCLICIARRLPRPPAITGVESFMTKQDTTGKIISID
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VSRGMTGNIGGQFGTGINPQMQQNVFQYPGAGMVPQCEANFAPSLSPGSSMVPMPIPP
PQSSLLQQTPPASGYQSPDMKAWQQGAIGNNNVFSQAVQNQPTPAQPGYYNNMSITVS
1151 TGATGACTCGTGGCACTGCCTCCTCCTATAGATTCATATTGAATGATGGGACAA 1210
                                                                                                                                                                                                                                                          1110 TAGTGACTGCACAGACAAAAAGCAAAACTCTTCCGAAATCCTGTAACAAATGATCGACATG 1169
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Homo saplens mRNA for steroid receptor coactivator le.
AJ000882
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                                                                                                                                  Length 4721;
                                                                                                                                                                       21;
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llarity 59.7%; Pred. No. 2.4e-68;
Conservative 0; Mismatches 406
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TSSLAAAGRTGWEDLVRKCIYAFFQPGREPSYRQLEYGEVWIRGTASSPSYRFILND
GTWLSAHTKCKLCYPQSPDWQPFIMGIHIDREHSGLESPQDDTNSGMSIPRVPPSVNP
SISPAHGARRSTLEPENSWYSTRINGQSSDLHSSSHSNSSNSGGSFGCSPGSUIV
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LTARHKILHRLLQEGSPSDITTLSVEPDKKDSASTSVSTGQVQGNSSIKLELDASKK
KESKOHQLLFYLLDKDEKDLESTPNLSLDDVKVVEKKEQDDPCNTNPTPWITPPTFF
KTEAQSQFTADLDOFDQLIPTLEKRAQLFOLCETDRMGAVTSVTIKSEILPASLQS
ATARPTSRLNRLPELELAIDNQFGOPGTGOD IPWTNNTVTAINQSKSEDQCISSQLD
ELLCPPTTVEGRNDEKALLEQLVSFLSGKDETELAELDRALGIDKLVGGGGLDVLSER
FPPQQATPPLIMEERPNLXSQPXSSFFPTANLPSFFQGWVRQKPSLGTMPVQVTPPRG
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PPNISTLSSPVGMTSSACNNNNRSYSNIPVTSLQGMNEGPNNSVGFSASSPVLROMSS
ONSPSRLNIQPAKAESKDNKEIASTLNEMIQSDNSSSDGKPLDSGLLHNNDRLSDGDS
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SSGLPVQTGNPRLPQGAPQOFPYPPNYGTNPGTPPASTSPFSQLAANPEASLANRNSM
VSRGMTGNIGGOFGTGINPQMQQNVFQYPGAGMVPQGEANFAPSLSPGSSMVPMPIPP
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MAGGNTNVQNMNPMMAQMQMSSLQMPGMNTVCPEQINDPALRHTGLYCNQLSSTDLLK
TEADGTQQVQQVQVFADVQCTVNLVGGDPYLNQPGPLGTQKPTSGPQTPQAQQKSLRQ
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Unpublished (1997)
Chases I to 4547)
Spencer.T.E., Jenster.G., Onate,S., Tsai,M.-J. and O'Malley,B.W.
Direct Submission
Submitted (34-FEB-1997) Cell Biology, Baylor College of Medicine,
M713 DeBakey Building, Houston, TX 77030, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 4547)
Spencer,T.E., Jenster,G., Onate,S., Tsal,M.-J. and O'Malley,B.W.
Cloning of full-length human steroid receptor coactivator-one
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TGATGACTCGTGGCACTGCCTCCAGCCCCTCTATAGATTCATATTGAATGATGGGACAA 1210
                                                                                                     TAGTGACTGCACAGACAAAAGCAAACTCTTCCGAAATCCTGTAACAAATGATCGACATG 1169
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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43. .4368
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Human steroid receptor coactivator-1 mRNA,
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/product="steroid receptor
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   DB 10; Length 4547;
                              Indels
 Score 328.4; DB 10;
Pred. No. 2.4e-68;
); Mismatches 406;
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Query Match 7.3
Best Local Similarity 59.7
Matches 633; Conservative
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156 CTCCAGGACAAGGTCTTACCTGCAGTGGTGAAAAACGGAGACGGGAGCAGGAAAGTAAAT 215 ò 셤

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573 AAGAAGACAGAAAGGATTTTCTTAAGAAT---TTACCAAAATCTACAGTTAATGGAGTTT 629

586

749 AAACACCACATGATATTCTGGAAGACATAAACGCCAGTCCTGAAATGCGCCAGAGATATG 069

698 AAGTAATGCAGTGTTTCACTGTGTCACAGCCAAAATCAATTCAAGTGGGGGAGGATT 757

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CAAACCCTGAGAGCTTTATTACCAGACATGATCTTTCAGGAAAGGTTGTCAATATAGATA 929 870

CAAATTCACTGAGATCCTCCATGAGGCCTGGCTTTGAAGATATAATCCGAAGGTGTATTC 989 930

990 AGAGATTTTTAGTCTAAATGATGGGCAGTCATGGTCCCAGAAACGTCACTATCAAGAAG 1049 .050 CITAICITAAIGGCCAIGCAGAAACCCCAGIAIATCGAIICICGIIGGCIGAIGGAACIA 1109 932

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1170 GCTTTGTCTCAACCCACTTCCTTCAGAGAACAGAATGG 1209 ò 셤

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

protein - protein database search, using Smith-Waterman algorithm MasPar time 56.90 Seconds 996.458 Million cell updates/sec Fri Sep 17 21:06:51 1999; Tabular output not generated. rch_pp

>US-09-041-994-2 (1-1415) from US09041994.pep 9849 Perfect Score: Description:

1 MSGLGENLDPLASDSRKRKL.....MNMNPMPMSGMPMGPDQKYC 1415 Sequence:

PAM 150 Gap 11 Scoring table:

122810 segs, 40068593 residues Searched:

Minimum Match 0% Listing first 45 summaries Post-processing:

pir60 Database:

1:pirl 2:pir2 3:pir3 4:pir4

Mean 55.130; Variance 137.576;

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scale 0.401

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Gaps

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7159

RAC3 #length 1417 #molecular-weight 154535 #checksum

#gene SUMMARY GENETICS

##residues___i______##label LIH ##cross-references EMBL:AF010227; NID:g2318005; PID:g2318006 ##experimental_source cell line HeLa

1. MSGLGENLDPLASDSRKRKLPCDTPGQGLTCSGEKRRREQESKYIEELAELISANLSDID 60

99.7%; Score 9815; DB 2; Length 1417; larity 99.7%; Pred. No. 0.00e+00; Conservative 1; Mismatches 1; Indels 2

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LDGFLFVVNREANIVEVSENVTQYLQYKQEDLVNTSVYNILHEEDRKDFLKNLPKSTVNG 180 121 LDGFLFVVNREANIVFVSENVTQYLQYKQEDLVNTSVYNILHEEDRKDFLKNLPKSTVNG 180

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181 VSWTNEPQRQKSHTFNCRWLMKTPHDILEDINASPEMRQRYETWQCFALSQPRAWMEEGE 240

181 VSWTNETOROKSHTFNCRMLMKTPHDILEDINASPEMRORYETMOCFALSOPRAMMEEGE 240

241 DLQSCMICVARRITIGERIFPSNPESFIIRHDISGKVVNIDINSLRSSMRPGFEDIIRRC 300

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301 IQRFFSLNDGQSWSQKRHYQEAYLNGHAETPVYRFSLADGTIVTAQTKSKLFRNPVTNDR 360

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	Description	receptor-associated c	probable nuclear rece	steroid receptor coac	aryl hydrocarbon rece	aryl hydrocarbon rece	alpha/beta-gliadin pr	transcription initiat	transcription factor	omega secalin precurs	secalin	transcription factor	hypothetical protein	aryl hydrocarbon rece	regulatory protein SN	ALR protein - human	ALR protein - human	odd-paired - fruit fl	homeotic protein cut	Mopa box protein - mo	Machado-Joseph diseas	involucrin - mouse	hypothetical protein	brain and muscle Ah r
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æ	Query Match	7.66	99.3	6.5	2.4	2.4	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.3	2.2	2.2	2.1	2.1	2.1	2.1	2.1
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JC3403 JQ1150 A53185 S25365 I53172 S66736	A43742 A374277 S39162 S39162 A46068 JC5406 JC5407 S074288	S21883 S27770 S27770 S47857 S60966 JC5809	receptor associated coactivator receptor associated coactivator 4. Mar-1999 #sequence_revision 24. Mar-1999 #sequence_revision 24. Mar-1999 #sequence_revision 703443	##label LIH
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Antick, S.L.; Kononen, J.; Walker, R.L.; Azorsa, D.O.;
Tanner, M.M.; Guan, X.Y.; Sauter, G.; Kallioniemi, O.
Trent, J.W.; Meltzer, P.S.
Science (1997) 277:965-968
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##cross-references EMBL:AF012108; NID:g2331249;
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Sequence and characterization of a coactivator
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Human arylhydrocarbon receptor: Functional expression and chromosomal assignment to 7p21.
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##Tesidues 1-4,'G',6-356,'H',358-460,'N',462-631,633-848 ##label
                                                                                                                                                                                                                                                    Dolwick, K.M.; Schmidt, J.V.; Carver, L.A.; Swanson, H.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           690 HONROAI-LNOFAATAPVGINMRSGMOOOITPOPPLNAOMLAORORELYSQOHRO-R-QL 746
                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                 456 MDGAVTSVTIKSEILPASLQSATARPTSRLN-RLPELELEAIDNQFGQPGTGDQI-PWTN
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                                                                                                                                                                                                                                                                                                                                                        514 NTVTAINQSK-SEDQCI-SSQLDELLCPPTTVEGRNDEKALLEQLVSFLSGKDETELAEL
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Nucleic Acids Res. (1993) 21:3578
Human Ah receptor cDNA: analysis for highly conserved
                                                       DB 2; Dec.,
1.76e-76;
-haq 89; Indels 21;
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   #checksum
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Cloning and expression of a human Ah receptor
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*sequence_revision 01-Mar-1996
   #molecular-weight 114166
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                                                                                                           Pred. No. 1.76e-89; Mismatches
                                                                          Score 643;
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Ah receptor
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15-Feb-1996 #sequence_revi
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NCE S41124
                                                                  ch 6.5%;
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113; Conservative
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Nucleic Acids Res. (1994) 22:3038-3044
Tissue specific expression of the rat Ah-receptor and ARNT
                                                                                                                                                                                                                                                                                                                                       84 -EQG-KIISNDDDVQKADVSSTG-QGVIDKDSLGPLLLQALDGFLFVVNREANIVFVSEN 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   $58375  #type complete aryl hydrocarbon receptor - rat Ah receptor #formal_name Rattus norvegicus #common_name Norway rat #formal_name Rattus norvegicus #common_name Norway rat 10.4pr.1996 #sequence_revision 19.4pr.1996 #text_change $58375; $62121
                                                                                                                                                                                                           Gaps
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#length 853 #molecular-weight 96220 #checksum 7010
                                                                                                             #region PAS domain
#length 848 #molecular-weight 96147 #checksum 8926
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submitted to the EMBL Data Library, April 1994
                                                                                                                                                                 Score 232; DB 2; Length 848;
Pred. No. 3.23e-14;
52; Mismatches 50; Indels
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##cross-references EMBL:U09000; NID:9510268; PID:9510269
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Best Local Similarity 30.9%; Pred. No. 3.62e-15;
Matches 47; Conservative 46; Mismatches 51; Indels
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                     ##cross-references GDB:138471; OMIM:600253
#map_position 7p21-7p15
KEYWORGS receptor
                                                                                                                                                                                                                                                                                                                                                                                                              141 VIQYLQYKQEDLVNISVYNILHEEDRKDFLKNL 173
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##residues 1-853 ##label CAR
##cross-references EMBL:U09000
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#accession S58375
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Best Local Similarity 27.5%;
Matches 42; Conservative
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Shewry, P.R.; Sabelli, P.A.; Parmar, S.; Lafiandra, D. Blochem. Genet. (1991) 29:207-211 alpha-type prolamins are encoded by genes on chromosomes 4Ha and 6Ha of Haynaldia villosa Schur (syn. Dasypyrum villosum
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                                                                                                                                                                                                                                                                                                               Sumner-Smith, M.; Rafalski, J.A.; Sugiyama, T.; Stoll, M.;
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S07924 *type complete
alpha/beta-gliadin precursor - wheat
*formal_name Triticum aestivum *common_name common wheat
08-Jun-1994 *sequence_revision 01-Dec-1995 *text_change
17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                    Soell, D.
Nucleic Acids Res. (1985) 13:3905-3916
Conservation and variability of wheat alpha/beta-gliadin
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Pred. No. 7.10e-13;
34; Mismatches 66; Indels
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##residues 1-339 ##label PET
##cross-references GB:M55654; NID:g339491; PID:g339492
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##cross-references EMBL:X02540; NID:g21764; PID:g21765
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Science (1990) 248:1646-1649
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A34830; A34831; S10944
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#accession 807924
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Best Local Similarity 32.9%;
Matches 53; Conservative
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##residues 1-3
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Cloning of a transcriptionally active human TATA binding
                                                                                                                                                  Roy, A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160128 #type complete
transcription factor IID - human
#formal_name Homo sapiens #common_name man
04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change
                                                                                                                                                                                                     Highly conserved core domain and unique N terminus with presumptive regulatory motifs in a human TATA factor
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Cloning of the human TATA binding factor: Expression
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#length 344 #molecular-weight 38409 #checksum 7457
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cross-references GB:M34960; NID:g339493; PID:g339494
:CATION #superfamily transcription initiation factor IID
                                                                                                                                              Hoffmann, A.; Sinn, E.; Yamamoto, T.; Wang, J.;
Horikoshi, M.; Roeder, R.G.
Nature (1990) 346:387-390
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                                                                      not compared with conceptual translation
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Pred. No. 2.82e-13;
16; Mismatches 49; Indels
                                                                                                           1-17,'N',19-186,'R',188-339 ##label KAO
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#length 339 #molecular-weight 37698
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#map_position 6q27-6q27
CLASSIFICATION #superfamily transcription initi
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               factor,
#cross-references MUID:90302010
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Best Local Similarity 38.5%;
Matches 42; Conservative
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Best Local Similarity 38.5%;
Matches 42; Conservative
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160128
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Gaps 15
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#journal Plant Mol. Biol. (1991) 17:1111-1115
#title Isolation and characterisation of genes encoding rye prolamins containing a highly repetitive sequence motif.
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Plant Mol. Blol. (1991) 17:111-1115
Isolation and characterisation of genes encoding rye
prolamins containing a highly repetitive sequence motif.
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#product omega secalin #status predicted #label MAT
#length 357 #molecular-weight 41541 #checksum 3278
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#formal_name Secale cereale #common_name rye
16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
08-Sep-1997
                                                                                                                                                                                                      #formal_name Secale cereale #common_name rye
16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 230; DB 2; Length 357;
Pred. No. 6.01e-14;
55; Mismatches 133; Indels 18;
                             1255 QQQQQQQQQQQQQTQAFSPPPNVTASPSMDGLLAGPTMPQAPPQQFPYQ 1303
77 QQQQQQQQQQQQQQQQQQAVAAAAVQQSTSQQATQGTSGQAPQLFHSQ 125
                                                                                                                                                   $18235 #type complete omega secalin precursor (clone pSec1B) - rye
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#superfamily gliadin
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Similarity 26.4%;
74; Conservative
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                                                                                                                                                                                                                                                                                                 72 QQPAPIQPQQPFPQQPQQPFPQPQQQLPLQPQQPFPQPQQPIPQQPQQSFPQQPQRPEQQ 131
                                                          #domain signal sequence #status predicted #label SIC #product omega secalin #status predicted #label MAT #length 357 #molecular-weight 41439 #checksum 3741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s39356  #type complete
transcription factor btd - fruit fly (Drosophila sp.)
#formal_name Drosophila sp.
18-Feb-1994 #sequence_revision 01-Dec-1995 #text_change
24-Sep-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S39356
Winner, E.A.; Jaeckle, H.; Pfeifle, C.; Cohen, S.M.
Nature (1993) 366:690-694
A Drosophila homologue of human Spl is a head-specific
                                                                                                                                                                                                                                                                                                                                                                                132 FPQQPQQIIPQQTQQPFPLQPQQPFPQQPQRSFAQQPKQIISQQPFPLQPQQPFSQPQQP
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hypothetical protein YM8520.13c
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                                                                                                                                     Score 229; DB 2; Length 357;
Pred. No. 8.19e-14;
45; Mismatches 117; Indels
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Local Similarity 28.2%;
les 71; Conservative
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1307 GMGQQPDPAFGR 1318
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##residues 1-6
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##residues 1-73,'S',75-131,'FL',134-170,'HV',173-805 ##label EMA ##experimental_source Hepa-1 cell residues 10-25 have been confirmed by protein sequencing A48601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##status preliminary
##molecule_type mRNA; protein
##residues 1-805 ##label BNR
##cross-references GB:M94623; NID:g405813; PID:g192101
##note sequence extracted from NCBI backbone (NCBIN:112849,
NCBIP:112851)
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#formal_name Saccharomyces cerevisiae
08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change
06-Feb-1998
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#journal Proc. Natl. Acad. Sci. U.S.A. (1992) 89:8185-8189
#title Cloning of the Ah-receptor cDNA reveals a distinctive
#cross-references MUID:92390411
                                                                                                                                                                                                                                                                                                                                                                                 #length 758 #molecular-weight 85050 #checksum 3135
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Molecular characterization of the murine Ahr gene. Organization, promoter analysis, and chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                               Length 758;
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Pred. No. 1.52e-13;
16; Mismatches 36; Indels
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                                                                                                              Hunt, S.; Bowman, S.
submitted to the EMBL Data Library,
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#map_position 13R
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A46266; JQ1485; A48601; A61274
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Best Local Similarity 44.6%;
Matches 45; Conservative
                                                                       S54522; S54609
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##molecule_type DNA
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This protein mediates biochemical and toxic effects of halogenated aromatic hydrocarbons.
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#journal Mol. Cell. Biol. (1990) 10:5616-5625
#title The SNF5 protein of Saccharomyces cerevisiae is a glutamine-and proline-rich transcriptional activator that affects expression of a broad spectrum of genes.
#cross-references MUID:91042489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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Yeast (1994) 10[Suppl.A]:S47-S62
The sequence of a 32420 bp segment located on the right arm of chromosome II from Saccharomyces cerevisiae.
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##cross-references EMBL:236158; NID:9536741; PID:9536742; MIPS:YBR289w
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                                                                                                        #authors Bradfield, C.A.; Glover, E.; Poland, A.
#journal Mol. Pharmacol. (1991) 39:13-19
#title Purification and N-terminal amino acid sequence of the Ah
receptor from the C57BL/6J mouse.
#cross-references MUID:91101622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S GGKTI-SNDDDVQKADVSSTGQGVIDKDSL--GPLILQALDGFLFVVNREANIVFVSENV 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 FDVALKSTPADRNGGQDQCRAQ-IRDWQDLQEGEFLLQALNGFVLVVTADALVFYASSTI 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                #checksum 8889
##molecule_type DNA
##residues 1-334 ##label SCH
##cross-references GB:L19749; GB:L19750; GB:L19751; GB:L19752;
##cross-references GB:L19753; GB:L19754; GB:L19755; GB:L19756
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RDS DNA binding; polymorphism; transcription factor
RY #length 805 #molecular-weight 90351 #checksum
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Pred. No. 4.40e-14;
46; Mismatches 52; Indels
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S44537
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                                                                                                                                                                                                                          ##molecule_type protein
##residues 10-36 ##label BRA
##experimental_source strain C57BL/6J
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Best Local Similarity 30.3%;
Matches 46; Conservative
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ALR protein - human
#formal_name Homo sapiens #common_name man
24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change
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Larity 28.5%; Pred. No. 4.40e-14;
Conservative 58; Mismatches 129; Indels 14
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##molecule_type mRNA
###rand...-
##residues 1-563,'D',565-905 ##label LAU ##cross-references GB:M36482; NID:g172637; PID:g172638
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    #region proline-rich
#length 905 #molecular-weight 102556
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em_est5::
em_est6::
em_est7::
em_est8::
em_est8::
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em_est2:*
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Perfect score:
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AA530243 vj38606.r
R28559 yh5bhl.rl
AA04419 zh5se06.r
AA300819 EST13767
AA062269 d07502m T
R21765 yh2la01.rl
R66357 yi34q11.rl
AA16619 UI-R-C1-k
AA360136 EST69252
C03704 C03704 Huma
AA823647 vr69b05.s
                                                                                                                                                                                                                                                                                                                                                                        H04364 Y120e11.r1
R21718 yh21e01.s1
R28355 yh25511.s1
R67499 yi33q11.s1
AA163058 ms24d10.r
AA619146 vo68e11.r
                                                                                                                                                                                                                                                                                                                                                                                                                                    Model5 yz86e06.s1
AI664474 ue62f06.r1
AA740705 ny98a04.s
RZ5318 yh42a0?
                                                                                                                                                         AA065270 e08802r T
AA114092 zn66e10.r
AA150333 2103e07.r
AA065271 203e02m T
AA065271 f08502r T
AA065272 c08502r T
AA065272 c08502r T
T77368 yd72908.r1
AA7440499 tr68e05.x
AA530243 vy38c06.r
RA53659 yh55b11.r1
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AA422600 vd28e04.s
AA744255 ny62g11.s
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F23060 SSC19F03 Po
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                                                                                                                                       AA488485 ab39a08.
W84822 zh53e05.rl
                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                        Description
                                                                                            SUMMARIES
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AA360136
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AA823647
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AA744255
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AA187197
AA939852
AI077892
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W84822
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em_est22:*
em_est23:*
em_est24:*
em_est25:*
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779.8
773.8
723.8
69.2
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2253.6
247.8
247.8
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247.8
1193.6
1193.6
1193.6
1194.4
1147.4
1146.2
1130.2
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353.8
347.6
343.4
316.4
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AA488485 547 bp mRNA EST 11-AUG-1997 ab39a08.rl Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone IMAGE:843158 5' similar to TR:G1314285 GR1814285 GRIP1 ;, mRNA

sequence. AA488485 g2215916

ACCESSION NID

RESULT 1 AA488485 LOCUS DEFINITION

ALIGNMENTS

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CAAGCAAC 3593
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AUTHORS
                         360
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                                                                                                                                                                                                                                   Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28m13 revi ET from Amersham
High quality, sequence stop: 445.
Location/Qualifiers
                                              Homosapiens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Mammalia;
Eutheria: Primates: Catarrhini: Hominidae: Homo.

1 (bases 1 to 547)
Hilliar.L. Allen.M., Bowles.L., Dubuque,T., Geisel,G., Jost,S., Kucaba.T., Lacy,M., Le.,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
Washg-Merck EST Project 1997
Unpublished (1997)
On Jan 25, 1995 this sequence version replaced gi:637866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCTCTTCTTAGGAATTCCCTGGATGATCTTGTTGGGCCACCTTCCAACCTGGAAGGCCA 3225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3106 GGGTTCCTGGCCCGATGCATGTTGTCCATGGAACAAGTTTCTCATGGCACTCAAAATAG 3165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3226 GAGIGACGAAAGAGCATTATTGGACCAGCTGCACTCTTCTCAGCAACACAGATGCGAC 3285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3406 GGCAGGATTATATGGACAGACATACCCAGCACAGGGGCCTCCAATGCAAGGAGGCTTTCA 3465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3346 ATTAGAGCCCAAACAGGATGCTTTCCAAGGCCAAGAAGCAGCAGTAATGATGGATCAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                         1. .547
/organism="Homo sapiens"
/db_xxef="texxon:9606"
/clone="ImAE:843158"
/clone_lib="Stratagene HeLa cell s3 937216"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 534.4; DB 34
Pred. No. 2.2e-135;
0; Mismatches 1;
      GI:2215916
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Best Local Similarity 99.6%;
Matches 546; Conservative C
AA488485.1
EST.
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                                      human.
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    VERSION
KEYWORDS
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                                                                                                              AUTHORS
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (Info@image.llnl.gov) for further information.
Seq primer: mob. REGAPET
High quality sequence stop: 312.
                                                                                                                                                                                                                                                                                                                                                                                                                        zh53e05.rl Soares_fetal_liver_spleen_lNFLS_S1 Homo sapiens cDNA clone IMAGE:415808 5', mRNA sequence.
                                                                 TCTTCAGGGACAATCACCATCTTTAACTCTATGATGAATCAGATGAACCAGCAAGGCAA 3525
27-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases to 437)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, E., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                         ITITCCTCTCCAAGGAATGCACCCACGAGCCAACATCATGAGACCCCGGACAAACACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .437 / Constitutes / Corganisms / Corganisms / Homo sapiens / Ab_xref="GDB:1324278" / Ab_xref="taxon:9606" / Clone="InAGE:415808" / Clone="InAGE:415808" / Clone="InAGE:415808" / Clone="InB="Soares_fetal_liver_spleen_lNFLS_SI" / Sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91:811263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The WashU-Merck EST Project
Unpublished (1995)
On May 18, 1995 this sequence version replaced
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Location/Qualifiers
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AA114092.1 GI:1667968
                                                                                                                                        Query Match 8.5%;
Best Local Similarity 97.8%;
Matches 397; Conservative
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                                                                                              112
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Unite INSERM 99, Hopital Henri Mondor, 94010 Creteil, France
Unite: (33)149913530
Fax: (33)148980908
Email: guellaen@infoblogen.fr
This sequence derives from a clone which was selected from the cDNA
library - Testis 5 - using a repeat of 14 CAG as probe
                          'n
                                                 4045
                                                                                                                                                                                                                                   4285
                                                                                                                                                                                                                                                                                                                          4225
                                                                                         ATGCCCATGTCTGGCATGCCTATGGGTCCTGATCAGAAATACTGCTGACATCTCTGCACC 4345
                                                                                                       Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                        180 TIGGCCAGGAACAGCICCTITICCCAGCAGCAGTITIGCCCACCAGGGGAAICCIGCAGIG
                                                                                                                                                                                                                                              3986 CCATATCAACCAAATTATGGAATGGGACAACAACCAGATCCAGCCTTTGGTCGAGTGTCT
                                                                                                                                       4106 CACCGCAGGCTGCATCCATCTATCAGTCCTCAGAAATGAAGGGCTGGCCATCAGGAAAT
                                                                                                                                                                                     TTGGCCAGGAACAGCTCCTTTTCCCAGCAGCAGTTTGCCCCACCAGGGGAATCCTGCAGTG
                                                                                                                                                                                                                                                                                         TATAGTATGGTGCACATGAATGGCAGCAGTGGTCACATGGGACAGATGAACATGAACCCC
                          4
  Length 437;
                          Indels
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   DB 26;
                         11;
Score 385.2; DB 2.
Pred. No. 1.3e-94;
0; Mismatches 11.
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/db_xref="taxon:9606"
/clone="e08502"
/clone_lib="Testis 5"
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Guellaen,G. Unpublished (1996)
Unpublished (1996)
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s 5 Homo s
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AA065270.1 GI:1929270
  8.68;
96.68;
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Unite INSERM 99
Query Match
Best Local Similarity 96.6
Matches 424; Conservative
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e08502r Testis
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AUTHORS
TITLE
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/note="Vector: pSPORT1; Site_1: Mlul; Site_2: Not1; mRNA was prepared from human testis of a 27 years old man. CDNA was prepared throw human testis of a 27 years old man. CDNA was prepared using a 15mer oligo dT anchored by two degenerated bases at its 3'end and containing a Not1 site at its 5'end. The CDNA was cloned between Sall and Not1 sites of pSPORT1. The Mlul·Sall fragement come from the adaptator used for the cloning. The 3' end is at the Not1 site. CDNA corresponding to abundant species were eliminated from this library." 2 others
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1 (bases 1 to 425)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Markins,M., Hullman,M., Kucaba,T., Lacy,M., Le,M., Le,M., E., Morris,M., Parsons,J., Parange,C., Rikin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mag,J., Travsskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA114092 425 bp mRNA EST 13-NOV-1996
zn66e10.rl Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone
IMAGE:563178 5' similar to TR:G726034 G726034 ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CTGGGTTCCTGGCCCGATGCATGTTGTCCATGGAACAAGTTTCTCATGGCACTCAAAAT 120
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Pred. No. 7.3e-94;
0; Mismatches 8; Indels
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Homo sapiens
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                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -28Mi3 rev2 from Amersham
High quality sequence stop: 354.
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 425;
                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:4592982"
/db_xref="taxon:9606"
/clone="InAGE:563178"
/clone_lib="Stratagene HeLa cell s3 937216"
/sex="female"
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                                              1 (bases 1 to 427)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chtapelli, B.,
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,
Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,
Trevaskis, E., Underwood, K., Soares, M.B., Tan, F., Thierry-Meg, J.,
and Marra, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Febr. 314 286 1810
Email: est@watson.wustl.edu
Hiff quality sequence stop: 381.
Location/qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                     Generation and analysis of 280,000 human expressed sequence Genome Res. 6 (9), 807-828 (1996)
97044478
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                                                                                                                                                                                                                                                                                                                                                            On May 9, 1995 this sequence version replaced gi:802993
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/clone_115="Soares_pregnant_uterus_NbHPU"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:3805855"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone==165502"
/clone==165502"
/clone==165502"
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/clone==165502"
/clone==16502"
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Fax: (33)148980908
Email: guellaen@infobiogen.fr
This sequence derives from a clone which was selected from the cDNA library - Testis 5 - using a repeat of 14 CAG as probe
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3540 GAATGCACCCACGA--GCCAACATCATGAGACCCCGGACAAACACCCCCAAGCAACTTAG 3597
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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5 Homo sapiens cDNA clone f05502 3' end, mRNA
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Pred. No. 2.4e-84;
0; Mismatches 11;
                                                                                                    1 (bases 1 to 405)
Guellaen, G.
Guellaen, G. Unpublished (1996)
Unpublished (1996)
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AA065268.1 GI:1929268
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Best Local Similarity 97.0%;
Matches 350; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: -21 M13.
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Unite INSERM 99
INSERM
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AA920142 457 bp mRNA EST 20-APR-1998 vy52g12.rl Stratagene mouse lung 937302 Mus musculus cDNA clone IMAGE:1299142 5' similar to TR:009000 009000 P300/CBP/CO-INTEGRATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 457)
Marra M., Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Marra M., Hiller, L., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                            4430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
4311 GTCCTGATCAGAAATACTGCTGACATCTCTGCACCAGGACCTCTTAAGGAAACCACTGTA 4370
                                                                                                                                                                                                                      4431 AGAAAGGACCAGCITIGAGCICCAICAAGGGIAITITAAGIGAIGICAITIGAGCAGGAA 4490
                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                         105 AGAAAGGACCAGCTTTGNGCTCCATCAAGGGTATTTAAGTGATGTCATTTGAGCAGGAC
                                                                                                         Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1407511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Possible reversed clone: similarity on wrong strand
Seq primer: -20mi3 revi Er from Amersham
High quality sequence stop: 410.
Location/Qualifiers
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/dev_stage="6-8 month old"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="C57BL/6 x CBA"
/db_xref="taxon:10090"
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Similarity
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Fax: (33)148980908
Email: quellaen@infobiogen.fr
This sequence derives from a clone which was selected from the cDNA
library - Testis 5 - using a repeat of 14 CAG as probe
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                                                                                        3058 GGGAATGGGGGCTAATCCCTATGGCCAAGCAGCATCTAACCAACTGGGTTCCTGGCC 3117
                                                                                                                                            3118 CGATGCCATGTTGTCCATGGAACAAGTTTCTCATGGCACTCAAAATAGGCCTCTTTTAG 3177
                                                                                                                                                                                                 3178 GAATICCCIGGAIGAICTIGTIGGGCCACCTICCAACCIGGAAGGCCAGAGIGACGAAAG 3237
                                                                                                                                                                                                                                                   3238 AGCATTATTGGACCAGCTGCACACTCTTCTCAGCAACACAGATGCGACAGGCCTGGAAGA 3297
                                                                                                                                                                                                                                                                                                                                                            3358 ACAGGATGCTTTCCAAGGCCAAGAAGCAGCAGTAATGATGGATCAGAAGGCAGGATTATA 3417
                                                                                                                                                                                                                                                                                                                                                                                                               3418 TGGACAGACATACCCAGCACAGGGGCCTCCAATGCAAGGAGGCTTTCATCTTCAGGGACA 3477
                                                                                                                                                                                                                                                                  181 AGCTCTGCTGGACCACCTGCACACACCTCTGAGCAACACAGATGCCACAGGTCTGGAGGA 240
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                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 405)
Guellaen, G.
Guellaen, G. Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA065271 405 bp mRNA EST 25-SEP-1996
f08502r Testis 5 Homo sapiens cDNA clone f08502 3' end, mRNA
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                                                                                                                                                            121 AAACTCTCTGGATGATCTGCGCCACCTTCTAACGCAGAGGCCAGAGTGACGAGAG
                                                                                                                                                                                                                                                                                                          AATTGACAGAGCTTTGGGCATTCCTGAACTTGTCAATCAGGGACAGGCATTAGAGCCCAA
                                                                ö
                                        Length 457;
                                                                Indels
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                                                               71;
                                      DB 40;
                                      Score 343.4; DB 4
Pred. No. 3.6e-83;
0; Mismatches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3478 ATCACCATCTTTTAACTCTATGATGAATCAGATGAAC 3514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 GTCACCATCGTTTAACTCTATGATGGGTCAGATTAGC 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                      7.68;
84.58;
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                                   Query Match
Best Local Similarity 84.5'
Matches 386; Conservative
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INSERM
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/clone_lb="restis 5"
/clone_lb="restis 5"
/clone_lb="restis 5"
/clone_lb="restis 5"
/clone_lb="restis of a 27 years old man. cDNA was prepared from human testis of a 27 years old man. cDNA was prepared using a 15mer oligo dT anchored by two degenerated bases at its 3'end and containing a NotI site at its 5'end. The cDNA was cloned between Sall and NotI sites of pSPORIL. The Miul.Sall fragement come from the adaptator used for the cloning. The 3' end is at the NotI site. cDNA corresponding to abundant species were eliminated from this library. I others
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9
                                                                                                                                                                                                                                                                                                                                                              7.0%; Score 316.4; DB 28; Length 405; llarity 91.8%; Pred. No. 8.2e-76; Conservative 0; Mismatches 27; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guellaen, G. Guellaen, G. Unpublished (1996)
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Fax: (33)148980908
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Best Local Similarity 99.1
Matches 333; Conservative
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Best Local Similarity
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                                                                                                          /organism="Homo sapiens"
//organism="Homo sapiens"
//db xref="taxon:9606"
//clone="c08500"
//clone=lib="trestis 5"
//clone="c08500"
//orde="Vector: pSPORTI; Site_1: Mlu1; Site_2: Not1; mRNA
was prepared from human testis of a 27 years old man. cDNA
was prepared using a 15mer oligo dr anchored by two
degenerated bases at its 3'end and containing a Not1 site
at its 5'end. The cDNA was cloned between Sall and Not1
sites of pSPORTI. The Mlu1. Sall fragement come from the
adaptator used for the cloning. The 3' end is at the Not1
site. cDNA corresponding to abundant species were
eliminated from this library."
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Email: guellaen@infoblogen.fr
This sequence derives from a clone which was selected from the cDNA
library - Testis 5 - using a repeat of 14 CAG as probe
Seq primer: M13 reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T77368 464 bp mRNA EST 15-MAR-1995 yd72g08.rl Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:113822 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3668 ATGGAAAACCCTACTGGTGGTGCTGCGGGTGATGAGGCCTATGATGAGCCCCAG--- 3725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3778 TCATC-ACTTCCGACAACAGGGGTGGCTATGATGATGCAGCAGCAGCAACAGCAGCAGC 3836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3608 CAGCAGAGGCTGCAGGCCAGCAGTTTTGAATCAGAGCCGACAGGCACTTGAATTGAAA 3667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3725 -----CAGGGTTTTCTTAATGC-TCAAATGGTCGCCCAACGCAGAGAAGGTGCTAAAG 3777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 464)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultan,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TITAACTCTATGATGAATCAGATGAACCAGCAAGGCAATTTTCCTCTCCAAGGAATGCAC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 309; DB 28; Length 405;
Pred. No. 8.7e-74;
0; Mismatches 10; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                         10 others
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                                                                                     Location/Qualifiers
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Best Local Similarity 94.3%;
Matches 364; Conservative (
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The Wash The Sarguence version replaced.

On Oct 24, 1994 this sequence version replaced.
Other ESTS: 1994 this sequence version replaced.
Other ESTS: 1994 this sequence version replaced.
Contact: Wilson RK Wash Mash Son The Wash Mash The Wash Mash The Wash Mash The Wash The Wash Mash The Wash The W
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Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P.
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/organism="Homo sapiens"
/db_xref="GDB:469439"
/db_xref="taxon:9606"
/clone="IMAGE:113822"
/clone_lib="Soares fetal liver spleen lNFLS"
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Pred..No. 2.7e-71;
0; Mismatches 0;
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Location/Qualifiers
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//dev_stage="14 weeks"
//dev_stage="4 weeks"
//dev_stage="0.000 weeks"
//dev_veekstage="0.000 weekstage="0.000 weekst
                                                                                                                                                                                                                                                                            Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 502)

Marram, Hillier, L., Allen, M., Bowles, M., Ditetrich, N., Dubuque, T., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Thelsing, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The Wash CHHMI Mouse EST Project
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AA764263 502 bp mRNA EST 27-JAN-1998 vv49f10.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:1225771 5' similar to TR:O09000 009000 P300/CBP/CO-INTEGRATOR PROTEIN. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3927 CCAGCATGGATGGCTTTTTGGCAGGACCCACAATGCCACAAGCTCCTCCGCAACAGTTTC 3986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
On May 8, 1995 this sequence version replaced gi:801107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 38; Length 502;
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Pred. No. 3.2e-71;
0; Mismatches 88;
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/sex="male"
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/db_xref="taxon:10090"
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                                                                                                                                                                                     AA764263.1 GI:2811785
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Best Local Similarity 80.3%;
Matches 363; Conservative (
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Sequencing Center
information can be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               è
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                         4285
                                                                                     ACCCGCAGGCTGCATCCATCTATCAGTCCTCAGAAATGAAGGGCTGGCCATCAGGAAATT 4166
                                                                                                                                                                                                                                                                                                                                                                                                                                          4286 ATGCCCATGTCTGGCATGCCTATGGGTCCTGATCAGAAATACTGCTGACATCTCTGCACC 4345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI440499 460 bp mRNA EST 18-MAR-1999
tc83e05.x1 NCI_CGAP_CLL1 Homo sapiens cDNA clone IMAGE:2072768
similar to TR:015406 015406 CAGH16.;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert-Strausbergenih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Cen
Clone distribution: NCI-CGAP clone distribution information cafound through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                     TGGCCAGGAACAGCTCCTTTTCCCAGCAGCAGTTTGCCCACGGGGAATCCTGCAGT-G 4225
                                                                                                                                                                                                                                       253 TGGCCAGGAATGGCTCCTTCCCCCAGCAGCAGTTTGCTCCCCAGGGGAACCCTGCAGCAGTCC 312
373 ATGCCCATGTCTGGCATGCCCATGGCCACGATCAGAAATACTGCTGACATCTCCCTAGT 432
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 460)
                                                                                                                                                                                                                                                                                                                                                           4226 TATAGTATGGTGCACATGAATGGCAGCAGTGGTCACATGGGACAGATGAACATGAACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo saplens"
/db_xref="taxon:9606"
/clone="IXAGE:2072768"
/clone=lib="NCLCGAP_CLL1"
/tlssue_type="B-cell, chronic lymphotic leukemia"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3188300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4346 AGGACCICITAAGGAAACCACIGIACAAAIGA 4377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433 GAGACTGACTGTACAGATGACACTGCACAGGA 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seg primer: -400P from Gibco
High quality sequence stop: 449.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 516)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                     ö
 the modified pT7T3 vector. constructed by Bento
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                             AA530243 516 bp mRNA EST 22-JUL-1997 vj3806.r1 Stratuagene mouse diaphragm (#937303) Mus musculus celone IMAGE:931306 5' similar to TR:G1336160 G1336160 STEROID RECEPTOR COACTIVATOR 1A. ;, mRNA sequence.
                                                                                                                                                                       Gaps
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Unpublished (1996)
On Sep 12, 1996 this sequence version replaced g1:1393273.
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                                                                                                                                Score 297.4; DB 46; Length 460;
Pred. No. 1.4e-70;
0; Mismatches 1; Indels 0;
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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the Not I and Eco RI sites of
Library is normalized, and was
Soares and M.Fatima Bonaldo."
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/db_xref="taxon:10090"
/clone="IMAGE:931306"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA530243.1 GI:2272949
                                                                                                                             Query Match 6.6%;
Best Local Similarity 99.7%;
Matches 298; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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AA530243
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AUTHORS
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R28559 323 bp mRNA EST 25-APR-1995
yh55b11.rl Soares placenta Nb2HP Homo sapiens cDNA clone
IMAGE:133629 5' similar to contains TAR1 repetitive element ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                       4056 AIGCAAIGAIGTCGICAAGAAIGGGICCCTCCCAGAAICCCAIGAIGCAACACCCGCAGG 4115
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                                                                                                                                                                                                                                                                                                                                                                                                         61 GIGCAATGATGATCAACAATGGGGCCTTCCCAGAATGCCATGGTGCAGCATCCTCAGC 120
                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 323)
Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 AIGGCTCCTTCCCCCAGCAGCAGTTGCTCCCCAGGGGAACCCTGCAGCCTACAACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CAAATTACGGAATGGGACAACCACCAGACCAGCCTTTGGTCGAGGCTCGAGTCCTCCCA
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444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                            Length 516;
                                                                                                                                                                                                                                Score 263.6; DB 34; Louis
Pred. No. 2.6e-61;
                                                                                                                                                                                                                                                                               0; Mismatches
                  /tissue_type="diaphragm"
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                                                                                                                                                                                                                                                                             Matches 308; Conservative
                                                                                                                                                                                                                                                               Similarity
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R28559
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R28559.1
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Search completed: September 18, 1999, 00:52:22
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AUTHORS
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/clone="libe"Soares placenta Nb2HP"
/clone_libe"Soares placenta Nb2HP"
/clone_libe"Soares placenta obtained at birth (full term)"
/dab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="Discrete" (ampicillin resistant)"
/lab_host=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4256
                                          Email: est@watson.wustl.edu
Insert Size: 630
Insert Langth: 630
Insert Length: 630
Seq primer: 0.00
Seq primer: Mi3RPl
High quality sequence stop: 314.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4137 CAGAAATGAAGGGCTGGCCATCAGGAAATTTGGCCAGGAACAGCTCCTTTTCCCAGCAGC 4196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4317 ATCAGAAATACTGCTGACATCTCTGCACCAGGACCTCTTAAGGAAACCACTGTACAAA-T 4375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAGAAATGAAGGGTGGCCATCAGGAAATTTGGCCAGGAACAGCTCCTTTTCCCAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4197 AGTTTGCCCACCAGGGGAATCCTGCAGTGTATAGTATGGTGCACATGAATGGCAGCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCACATGGGACAGATGAACATGAACCCCATGCCCATGTCTGGCATGCCTATGGGTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GTCACATGGGACAGATGAACATGAACCCCATGCCCATGTCTGGCATGCCTATGGGTCCTG
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5.6%; Score 252.8; DB 22; Length 323;
Best Local Similarity 97.5%; Pred. No. 1.8e-58;
Matches 277; Conservative 0; Mismatches 4; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4376 GACACTGCACTAGGATTATTGGG--AAGGAATCATTGTTCCAGG 4417
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                     FEATURES
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Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Recaba, T., Lacy, M., Le, N., Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J., Treyaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation and analysis of 280,000 human expressed sequence tags of 200,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Feat: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
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IMAGE Consortum (info@image.llnl.gov) for further information.
Insert Length: 1867 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 232.
Location/Qualifilers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 ATTIGGCCAGGAACAGCTCCTTTTCCCAGCAGCAGTTTGCCCACCAGGGGAATCCTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3985 TCCATATCAACCAAATTATGGAAT-GGGACAACAACAGGATCCAGCCTTTGGTCGAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCCATATCAACCAAATTATGGAATCGGGACAACCAGATCCAGGCTTTGGTCGAGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4164 ATTTGGCCAGGAACAGCTCCTTTTCCCAGCAGCAGTTTGCCCACCAGGGGAATCCTGCAG
                                                                                                                                                                                                                                                        On Jan 25, 1995 this sequence version replaced g1:637753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>ښ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4224 TGTATAGTATGGTGCACATGAA-TGGCAGCAGTGGTCACATGGGACAG 4270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="GDB:3760818"
/db_xref="taxon:9606"
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/clone=lib="Soares_pregnant_uterus_NbHPU"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 247.8; DB
Pred. No. 4e-57;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.58;
                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 97.9
Matches 282; Conservative
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us-09-041-994-1.rst

Job time: 20100 sec

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